

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run On: December 14, 2002, 05:21:11 ; Search time 60 seconds
(without alignments)
7666.919 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgccggtgcgag.....tgacgaggctaaccagtga 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	246	16.4	2880	1	US-08-462-484-3
2	246	16.4	2880	1	US-08-441-147-3
3	246	16.4	2880	5	PCT-US95-07536-3
4	38	2.5	2418	1	US-08-462-484-1
5	38	2.5	2418	1	US-08-441-147-1
6	38	2.5	2418	5	PCT-US95-07536-1
7	35	2.3	2925	1	US-08-462-484-9
8	35	2.3	2925	5	PCT-US95-07536-9
9	35	2.3	2925	1	US-08-441-147-9
10	30	2.0	2860	1	US-08-462-484-7
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12	30	2.0	2860	5	PCT-US95-07536-7
13	24	1.6	3102	1	US-08-462-484-5
14	24	1.6	3102	1	US-08-441-147-5
15	24	1.6	3102	5	PCT-US95-07536-5
16	21	1.4	1161	3	US-08-689-421-22
17	21	1.4	1161	4	US-09-389-528-22
18	21	1.4	1161	4	US-09-181-827A-22
19	21	1.4	2940	3	US-08-689-421-28
20	21	1.4	2940	4	US-09-389-528-28
21	21	1.4	2940	4	US-09-181-827A-28
22	20	1.3	533	4	US-09-198-119C-66
23	20	1.3	768	4	US-09-198-119C-58
24	19	1.3	1088	3	US-09-040-885A-1
25	19	1.3	2009	1	US-07-958-222A-1
26	18	1.2	1155	4	US-08-818-112-12
27	18	1.2	1155	4	US-08-818-111-12

28 18 1.2 1155 4 US-09-056-556-12 Sequence 12, Appl
29 18 1.2 1155 4 US-09-072-596-12 Sequence 12, Appl
30 18 1.2 2574 4 US-09-255-829-27 Sequence 27, Appl
31 17 1.1 17 1 US-08-526-964-6 Sequence 6, Appl
32 17 1.1 17 2 US-08-946-617-6 Sequence 6, Appl
33 17 1.1 17 4 US-09-080-625-16 Sequence 16, Appl
34 17 1.1 17 4 US-09-695-782-16 Sequence 16, Appl
35 17 1.1 18 4 US-08-898-180-15 Sequence 15, Appl
36 17 1.1 19 4 US-09-115-475-4 Sequence 4, Appl
37 17 1.1 20 3 US-08-750-145A-12 Sequence 12, Appl
38 17 1.1 20 3 US-08-975-698A-9 Sequence 9, Appl
39 17 1.1 20 3 US-08-873-437-3 Sequence 3, Appl
40 17 1.1 20 4 US-09-417-090-9 Sequence 9, Appl
41 17 1.1 20 4 US-09-727-578-9 Sequence 9, Appl
42 17 1.1 20 4 US-09-662-235-5 Sequence 5, Appl
43 17 1.1 22 1 US-08-033-837A-3 Sequence 3, Appl
44 17 1.1 22 1 US-08-374-983A-3 Sequence 3, Appl
45 17 1.1 24 3 US-09-126-280-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-462-484-3
; Sequence 3, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Balboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Kasylyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56675310 No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441.147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowrey, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/POCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron

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; LOCATION: 837..899
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1014..1066
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1133..1187
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1284..1342
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1752..1815
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1873..1928
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2136..2195
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(364..543, 593..661, 716..835, 900..1013,
; LOCATION: 1067..1132, 1188..1283, 1343..1498, 1554..1751,
; LOCATION: 1816..1872, 1929..2135, 2196..2489)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 662..715
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1499..1553
; US-08-462-484-3

Query Match 16.4%; Score 246; DB 1; Length 2880;
Best Local Similarity 99.7%; Pred. No. 5.4e-106;
Matches 296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1204 CAGCCCTTCGCGGTTCGTCAGCGGGGAGCACACGATATACTACACGACCCGATC 1263
Db 2196 CAGCCCTTCGCGGTTCGTCAGCGGGGAGCACACGATATACTACACGACCCGATC 2255

Qy 1264 TTCGGCAGCTCGTGACGACGGGACGCGCGGGGACACGTCAGATCCGCTTC 1323
Db 2256 TTCGGCAGCTCGTGACGACGGGACGCGCGGGGACACGTCAGATCCGCTTC 2315

Qy 1324 CAGACGACAAACCCCGGCGGTGTCTCCACTGCGACATCGACTTCCACCTCGACGCG 1383
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Qy 1384 GGCTTCGCGATCGTTCGACAGGAGCGTTGCGGACGTGAGGCGGCGAACCCTTCG 1443
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Qy 1444 AAGCGGTGTCGACCTGTCCCGATCTAGACGGGCTGAGCGAGGCTAACAGTGA 1500
Db 2436 AAGCGGTGTCGACCTGTCCCGATCTAGACGGGCTGAGCGAGGCTAACAGTGA 2492

RESULT 2
US-08-441-147-3
; Sequence 3, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalborge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5770418a No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
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; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron
; LOCATION: 837..899
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1014..1066
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1133..1187
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1284..1342
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1752..1815
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1873..1928
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2136..2195
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(364..543, 593..661, 716..835, 900..1013,
; LOCATION: 1067..1132, 1188..1283, 1343..1498, 1554..1751,
; LOCATION: 1816..1872, 1929..2135, 2196..2489)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 662..715
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1499..1553
; US-08-441-147-3

Query Match 16.4%; Score 246; DB 1; Length 2880;
Best Local Similarity 99.7%; Pred. No. 5.4e-106;
Matches 296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1204 CAGCCCTTCGCGGTTCGTCAGCGGGGAGCACACGATATACTACACGACCCGATC 1263
Db 2196 CAGCCCTTCGCGGTTCGTCAGCGGGGAGCACACGATATACTACACGACCCGATC 2255

Qy 1264 TTCGGCAGCTCGTGACGACGGGACGCGCGGGGACACGTCAGATCCGCTTC 1323
Db 2256 TTCGGCAGCTCGTGACGACGGGACGCGCGGGGACACGTCAGATCCGCTTC 2315

Qy 1324 CAGACGACAAACCCCGGCGGTGTCTCCACTGCGACATCGACTTCCACCTCGACGCG 1383
Db 2316 CAGACGACAAACCCCGGCGGTGTCTCCACTGCGACATCGACTTCCACCTCGACGCA 2375

Qy 1384 GGCTTCGCGATCGTTCGACAGGAGCGTTGCGGACGTGAGGCGGCGAACCCTTCG 1443
Db 2376 GGCTTCGCGATCGTTCGACAGGAGCGTTGCGGACGTGAGGCGGCGAACCCTTCG 2435

Qy 1444 AAGCGGTGTCGACCTGTCCCGATCTAGACGGGCTGAGCGAGGCTAACAGTGA 1500
Db 2436 AAGCGGTGTCGACCTGTCCCGATCTAGACGGGCTGAGCGAGGCTAACAGTGA 2492
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;; FILING DATE: 15-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lowney, Karen A.
;; REGISTRATION NUMBER: 31,274
;; REFERENCE/DOCKET NUMBER: 4185.010-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 867 0123
;; TELEFAX: 212 878 9635
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2418 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Polyporus pinsitus
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 414..464
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 534..589
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 710..764
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 879..934
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1001..1050
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1147..1197
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1354..1410
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1609..1662
;; NAME/KEY: CDS
;; LOCATION: join (413..465, 533..590, 709..765, 878..935,
;; LOCATION: 1000..1051, 1146..1198, 1353..1411, 1608..1663)
US-08-462-484-1

Query Match 2.5% Score 38; DB 1; Length 2418;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 1379
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Db 2065 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 2102

RESULT 5
US-08-441-147-1
; Sequence 1, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York

;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/441.147
;; FILING DATE: 15-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lowney, Karen A.
;; REGISTRATION NUMBER: 31,274
;; REFERENCE/DOCKET NUMBER: 4185.010-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 867 0123
;; TELEFAX: 212 878 9655
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2418 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Polyporus pinsitus
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 414..464
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 534..589
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 710..764
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 879..934
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1001..1050
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1147..1197
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1354..1410
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 1609..1662
;; NAME/KEY: CDS
;; LOCATION: join (413..465, 533..590, 709..765, 878..935,
;; LOCATION: 1000..1051, 1146..1198, 1353..1411, 1608..1663)
US-08-441-147-1

Query Match 2.5% Score 38; DB 1; Length 2418;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 1379
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Db 2065 CCGTGGTTCTCCACTGCCACATCGACTTCCACCTCGA 2102

RESULT 6
PCT-US95-07536-1
; Sequence 1, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07536
FILING DATE: 15-June-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,534
FILING DATE: 24-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.204-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2418 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Polyporus pinsitus
FEATURE:
NAME/KEY: intron
LOCATION: 414..464
FEATURE:
NAME/KEY: intron
LOCATION: 534..589
FEATURE:
NAME/KEY: intron
LOCATION: 710..764
FEATURE:
NAME/KEY: intron
LOCATION: 879..934
FEATURE:
NAME/KEY: intron
LOCATION: 1001..1050
FEATURE:
NAME/KEY: intron
LOCATION: 1147..1197
FEATURE:
NAME/KEY: intron
LOCATION: 1354..1410
FEATURE:
NAME/KEY: intron
LOCATION: 1609..1662
FEATURE:
NAME/KEY: CDS
LOCATION: join (413..465, 533..590, 709..765, 878..935,
1000..1051, 1146..1198, 1353..1411, 1608..1663)
PCT-US95-07536-1

Query Match 2.5% Score 38; DB 5; Length 2418;
Best Local Similarity 100.08; Pred. No. 1.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
DB 2065 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 2102

RESULT 7
US-08-462-484-9
Sequence 9, Application US/08462484
Patent No. 5667531
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Xu, Feng
APPLICANT: Dalboge, Henrik
APPLICANT: Schneider, Falle
APPLICANT: Aslsyng, Dorrit A.
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,484
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,147
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Polyporus pinsitus
FEATURE:
NAME/KEY: intron
LOCATION: 734..808
FEATURE:
NAME/KEY: intron
LOCATION: 878..932
FEATURE:
NAME/KEY: intron
LOCATION: 1051..1104
FEATURE:
NAME/KEY: intron
LOCATION: 1219..1270
FEATURE:
NAME/KEY: intron
LOCATION: 1336..1397
FEATURE:
NAME/KEY: intron
LOCATION: 1713..1744
FEATURE:
NAME/KEY: intron
LOCATION: 2030..2085
FEATURE:
NAME/KEY: intron
LOCATION: 2308..2375

; FEATURE: intron
; NAME/KEY: intron
; LOCATION: 2492..2569
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (733..809, 877..933, 1050..1105, 1218..1271,
; LOCATION: 2542..2600).
; US-08-462-484-9

Query Match 2.3%; Score 35; DB 1; Length 2925;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 1376
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Db 2587 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 2621

RESULT 8
US-08-441-147-9
; Sequence 9, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Xaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palie
; APPLICANT: Aaslynd, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus
; FEATURE:
; NAME/KEY: intron
; LOCATION: 734..808
; FEATURE:
; NAME/KEY: intron
; LOCATION: 878..932
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1051..1104
; FEATURE:

; NAME/KEY: intron
; LOCATION: 1219..1270
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; LOCATION: 1336..1397
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; LOCATION: 2030..2085
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (733..809, 877..933, 1050..1105, 1218..1271,
; LOCATION: 2542..2600).
; US-08-441-147-9

Query Match 2.3%; Score 35; DB 1; Length 2925;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 2587 CCGTGGTTCTCCACTGCCACATCGACTTCCACCT 2621

RESULT 9
PCT-US95-07536-9
; Sequence 9, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07536
; FILING DATE: 15-June-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/265,534
; FILING DATE: 24-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus

FEATURE:
NAME/KEY: intron
LOCATION: 734..808
FEATURE:
NAME/KEY: intron
LOCATION: 878..932
FEATURE:
NAME/KEY: intron
LOCATION: 1051..1104
FEATURE:
NAME/KEY: intron
LOCATION: 1219..1270
FEATURE:
NAME/KEY: intron
LOCATION: 1336..1397
FEATURE:
NAME/KEY: intron
LOCATION: 1713..7744
FEATURE:
NAME/KEY: intron
LOCATION: 2030..2085
FEATURE:
NAME/KEY: intron
LOCATION: 2308..2375
FEATURE:
NAME/KEY: intron
LOCATION: 2492..2569
FEATURE:
NAME/KEY: CDS
LOCATION: join (733..809, 877..933, 1050..1105, 1218..1271, 2542..2600).
PCT-US95-07536-9

Query Match 2.3%; Score 35; DB 5; Length 2925;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 CGTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 2587 CGTGGTTCCTCCACTGCCACATCGACTTCCACCT 2621

RESULT 10

US-08-462-484-7

Sequence 7, Application US/08462484

Patent No. 5667531

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue

APPLICANT: Xu, Feng

APPLICANT: Dalboge, Henrik

APPLICANT: Schneider, Palle

APPLICANT: Aaslyng, Dorrit A.

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,484

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/441,147

FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lowrey, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.010-US
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2860 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: intron
LOCATION: 851..905
FEATURE:
NAME/KEY: intron
LOCATION: 1266..1320
FEATURE:
NAME/KEY: intron
LOCATION: 1351..1376
FEATURE:
NAME/KEY: intron
LOCATION: 1416..1468
FEATURE:
NAME/KEY: intron
LOCATION: 1625..1683
FEATURE:
NAME/KEY: intron
LOCATION: 1882..1934
FEATURE:
NAME/KEY: intron
LOCATION: 2202..2252
FEATURE:
NAME/KEY: intron
LOCATION: 2370..2425
FEATURE:
NAME/KEY: intron
LOCATION: 2543..2599
FEATURE:
NAME/KEY: CDS
LOCATION: join(540..725, 782..850, 906..1025, 1086..1265, 1321..1350, 1377..1415, 1469..1624, 1684..1881, 1935..2201, 2253..2369, 2426..2542, 2600..2653)
US-08-462-484-7

Query Match 2.0%; Score 30; DB 1; Length 2860;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1345 TGGTTCTCCACTGCCACATCGACTTCCAC 1374
|||||

Db 2444 TGGTTCTCCACTGCCACATCGACTTCCAC 2473

RESULT 11

US-08-441-147-7

Sequence 7, Application US/08441147

Patent No. 5770418

GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue

APPLICANT: Xu, Feng

APPLICANT: Dalboge, Henrik

APPLICANT: Schneider, Palle

APPLICANT: Aaslyng, Dorrit A.

TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND

NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5770418o No. 5770418disk of No. 5770418th America, Inc.

STREET: 405 Lexington Avenue, Suite 6400

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,147
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.010-US
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2860 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: intron
LOCATION: 851..905
FEATURE:
NAME/KEY: intron
LOCATION: 1266..1320
FEATURE:
NAME/KEY: intron
LOCATION: 1351..1376
FEATURE:
NAME/KEY: intron
LOCATION: 1416..1468
FEATURE:
NAME/KEY: intron
LOCATION: 1625..1683
FEATURE:
NAME/KEY: intron
LOCATION: 1882..1934
FEATURE:
NAME/KEY: intron
LOCATION: 2202..2252
FEATURE:
NAME/KEY: intron
LOCATION: 2370..2425
FEATURE:
NAME/KEY: intron
LOCATION: 2543..2599
FEATURE:
NAME/KEY: CDS
LOCATION: join(540..725, 782..850, 906..1025, 1086..1265,
1321..1350, 1377..1415, 1469..1624, 1684..1881,
1935..2201, 2253..2369, 2426..2542, 2600..2653)
US-08-441-147-7

Query Match 2.0%; Score 30; DB 1; Length 2860;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1345 TGGTTCCTCCACTGCCACATCGACTTCCAC 1374
|||||

Db 2444 TGGTTCCTCCACTGCCACATCGACTTCCAC 2473
|||||

RESULT 12
PCT-US95-07536-7
Sequence 7, Application PC/TUS9507536
GENERAL INFORMATION:

APPLICANT:
APPLICANT:
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07536
FILING DATE: 15-June-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,534
FILING DATE: 24-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.204-WO
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2860 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: intron
LOCATION: 851..905
FEATURE:
NAME/KEY: intron
LOCATION: 1266..1320
FEATURE:
NAME/KEY: intron
LOCATION: 1351..1376
FEATURE:
NAME/KEY: intron
LOCATION: 1416..1468
FEATURE:
NAME/KEY: intron
LOCATION: 1625..1683
FEATURE:
NAME/KEY: intron
LOCATION: 1882..1934
FEATURE:
NAME/KEY: intron
LOCATION: 2202..2252
FEATURE:
NAME/KEY: intron
LOCATION: 2370..2425
FEATURE:
NAME/KEY: intron
LOCATION: 2543..2599
FEATURE:
NAME/KEY: CDS
LOCATION: join(540..725, 782..850, 906..1025, 1086..1265,
1321..1350, 1377..1415, 1469..1624, 1684..1881,
1935..2201, 2253..2369, 2426..2542, 2600..2653)
PCT-US95-07536-7

Query Match 2.0%; Score 30; DB 5; Length 2860;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1345 TGGTTCCTCCACTGCCACATCGACTTCCAC 1374


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FEATURE:
NAME/KEY: intron
LOCATION: 790..845
FEATURE:
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LOCATION: 1125..1182
FEATURE:
NAME/KEY: intron
LOCATION: 1390..1450
FEATURE:
NAME/KEY: intron
LOCATION: 1607..1661
FEATURE:
NAME/KEY: intron
LOCATION: 1863..1918
FEATURE:
NAME/KEY: intron
LOCATION: 1976..2025
FEATURE:
NAME/KEY: intron
LOCATION: 2227..2285
FEATURE:
NAME/KEY: intron
LOCATION: 2403..2458
FEATURE:
NAME/KEY: intron
LOCATION: 2576..2627
FEATURE:
NAME/KEY: CDS
LOCATION: join (665..721, 789..846, 1124..1183, 1389..1451,
LOCATION: 1606..1662, 1862..1919, 1975..2026, 2226..2286, 2402..2459,
LOCATION: 2575..2628).
US-08-441-147-5

Query Match          1.6%; Score 24; DB 1; Length 3102;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 ATCAACTCCGCCATCCTGCGCTAC 843
      |||||
Db 1754 ATCAACTCCGCCATCCTGCGCTAC 1777

RESULT 15
PCT-US95-07536-5
Sequence 5, Application PC/TUS9507536
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07536
FILING DATE: 15-June-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,534
FILING DATE: 24-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185,204-WO
TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Polyporus pinsitus
FEATURE:
NAME/KEY: intron
LOCATION: 666..720
FEATURE:
NAME/KEY: intron
LOCATION: 790..845
FEATURE:
NAME/KEY: intron
LOCATION: 1125..1182
FEATURE:
NAME/KEY: intron
LOCATION: 1390..1450
FEATURE:
NAME/KEY: intron
LOCATION: 1607..1661
FEATURE:
NAME/KEY: intron
LOCATION: 1863..1918
FEATURE:
NAME/KEY: intron
LOCATION: 1976..2025
FEATURE:
NAME/KEY: intron
LOCATION: 2227..2285
FEATURE:
NAME/KEY: intron
LOCATION: 2403..2458
FEATURE:
NAME/KEY: intron
LOCATION: 2576..2627
FEATURE:
NAME/KEY: CDS
LOCATION: join (665..721, 789..846, 1124..1183, 1389..1451,
LOCATION: 1606..1662, 1862..1919, 1975..2026, 2226..2286, 2402..2459,
LOCATION: 2575..2628).
PCT-US95-07536-5

Query Match          1.6%; Score 24; DB 5; Length 3102;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 ATCAACTCCGCCATCCTGCGCTAC 843
      |||||
Db 1754 ATCAACTCCGCCATCCTGCGCTAC 1777

Search completed: December 14, 2002, 06:56:05
Job time : 117 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 06:53:32 ; Search time 65 Seconds
(without alignments)
9126.023 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgccggtggcgag.....tgagcgaggtaaccagtga 1500

Scoring table: Oligo_NUC
Gapop 60.0 , Gapext 60.0

Searched: 355320 seqs, 197730502 residues

Word size : 0

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
 - 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
 - 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
 - 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
 - 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	1.4	590	10	US-09-917-800A-1579
c 2	20	1.3	533	9	US-09-996-140-66
c 3	20	1.3	768	9	US-09-996-140-58
c 4	19	1.3	1383	10	US-09-815-242-9610
c 5	19	1.3	1749	10	US-09-923-779-149
c 6	19	1.3	1864	9	US-09-974-298-43
c 7	19	1.3	1892	12	US-10-044-090-793
c 8	19	1.3	3405	9	US-09-974-298-44
c 9	19	1.3	3405	9	US-09-981-353-36
10	18	1.2	227	10	US-09-294-093B-4004
11	18	1.2	273	10	US-09-294-093B-3898
12	18	1.2	1503	9	US-09-712-363-128
c 13	18	1.2	397658	10	US-09-813-320-3
14	17	1.1	17	10	US-09-946-376-2
15	17	1.1	18	10	US-09-855-999-15
16	17	1.1	19	9	US-09-341-600A-4
17	17	1.1	22	10	US-09-775-217-20
18	17	1.1	24	10	US-09-738-769A-19
c 19	17	1.1	33	9	US-09-951-052A-10

ALIGNMENTS

RESULT 1
US-09-917-800A-1579
; Sequence 1579, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917.800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1579
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012838
US-09-917-800A-1579

Sequence 7, Appli
Sequence 3459, Ap
Sequence 4, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3335, Ap
Sequence 3334, Ap
Sequence 7717, Ap
Sequence 9, Appli
Sequence 713, App
Sequence 659, App
Sequence 675, App
Sequence 6, Appli
Sequence 2, Appli
Sequence 808, App
Sequence 7, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 24463, A
Sequence 693, App

Query Match 1.3%; Score 19; DB 10; Length 1383;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SEQ ID NO 9610
LENGTH: 1383
TYPE: DNA
ORGANISM: Salmonella typhi
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1383)
NAME/KEY: misc_feature
LOCATION: (1)...(1383)
OTHER INFORMATION: n = A,T,C or G
US-09-815-242-9610

Query Match 1.3%; Score 19; DB 10; Length 1383;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 GACTTTCACGCCGCCGACC 1044
|||||

DB 1104 GACTTTCACGCCGCCGACC 1086
|||||

RESULT 5

US-09-923-779-149/c

Sequence 149, Application US/09923779

Patent No. US20020076721A1

GENERAL INFORMATION:

APPLICANT: Pyle, Ruth A.

APPLICANT: Xu, Jiangchun

APPLICANT: Kalos, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.553

CURRENT APPLICATION NUMBER: US/09/923,779

CURRENT FILING DATE: 2001-08-06

NUMBER OF SEQ ID NOS: 155

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 149

LENGTH: 1749

TYPE: DNA

ORGANISM: Homo sapiens

US-09-923-779-149

Query Match 1.3%; Score 19; DB 10; Length 1749;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||

DB 812 TCCACCTCGACGGCGCTT 794
|||||

RESULT 6

US-09-974-298-43/c

Sequence 43, Application US/09974298

Patent No. US20020156263A1

GENERAL INFORMATION:

APPLICANT: Chen, Hwei-Mei

TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER

FILE REFERENCE: PA-0037 P

CURRENT APPLICATION NUMBER: US/09/974,298

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/238,331

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PERL Program

SEQ ID NO 43

LENGTH: 1864

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20020156263A1 127987.19

US-09-974-298-43

Query Match 1.3%; Score 19; DB 9; Length 1864;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||

DB 660 TCCACCTCGACGGCGCTT 642
|||||

RESULT 7

US-10-044-090-793/c

Sequence 793, Application US/10044090

Patent No. US20020137081A1

GENERAL INFORMATION:

APPLICANT: Olga Bandman

TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

FILE REFERENCE: PA-0028 US

CURRENT APPLICATION NUMBER: US/10/044,090

CURRENT FILING DATE: 2002-01-09

NUMBER OF SEQ ID NOS: 850

SOFTWARE: PERL Program

SEQ ID NO 793

LENGTH: 1892

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20020137081A1 2812002CB1

US-10-044-090-793

Query Match 1.3%; Score 19; DB 12; Length 1892;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||

DB 675 TCCACCTCGACGGCGCTT 657
|||||

RESULT 8

US-09-974-298-44/c

Sequence 44, Application US/09974298

Patent No. US20020156263A1

GENERAL INFORMATION:

APPLICANT: Chen, Hwei-Mei

TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER

FILE REFERENCE: PA-0037 P

CURRENT APPLICATION NUMBER: US/09/974,298

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/238,331

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PERL Program

SEQ ID NO 44

LENGTH: 3405

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20020156263A1 1397781.7

US-09-974-298-44

Query Match 1.3%; Score 19; DB 9; Length 3405;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGCGCTT 1388
|||||

DB 802 TCCACCTCGACGGCGCTT 784
|||||

RESULT 9

US-09-981-353-36/c
; Sequence 36, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 3405
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 1397781.7
US-09-981-353-36

Query Match 1.3%; Score 19; DB 9; Length 3405;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1370 TCCACCTCGACGGGGCTT 1388
|||||
DB 802 TCCACCTCGACGGGGCTT 784

RESULT 10
US-09-294-093B-4004
; Sequence 4004, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalugudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 4004
; LENGTH: 227
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700352953H1
US-09-294-093B-4004

Query Match 1.2%; Score 18; DB 10; Length 227;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 CAAGCGCACGAGTCGCC 861
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DB 185 CAAGCGCACGAGTCGCC 202

RESULT 11
US-09-294-093B-3898
; Sequence 3898, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalugudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3898
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700352769H1
US-09-294-093B-3898

Query Match 1.2%; Score 18; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 CAAGCGCACGAGTCGCC 861
|||||
DB 185 CAAGCGCACGAGTCGCC 202

RESULT 12
US-09-712-363-128
; Sequence 128, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Edward M.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-128

Query Match 1.2%; Score 18; DB 9; Length 1503;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1146 CACGCTGCCCGCACCGC 1163
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DB 820 CACGCTGCCCGCACCGC 837

RESULT 13

US-09-813-320-3/c
; Sequence 3, Application US/09813320
; Patent No. US20020142378A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Hongyu et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001172
; CURRENT APPLICATION NUMBER: US/09/813,320
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 397658
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(397658)
; OTHER INFORMATION: n = A,T,C or G
US-09-813-320-3

Query Match 1.2%; Score 18; DB 10; Length 397658;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 CACGGCTTCTCCAGGCA 213

Db 100446 CACGGCTTCTCCAGGCA 100429

RESULT 14

US-09-946-376-2
; Sequence 2, Application US/09946376
; Patent No. US2002015146A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Jae-Gu
; APPLICANT: Jung, Hueng-Chae
; TITLE OF INVENTION: Method of Protein Synthesis
; FILE REFERENCE: 10981-003-999
; CURRENT APPLICATION NUMBER: US/09/946,376
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 00-52464
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-946-376-2

Query Match 1.1%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 662 TCGAGGTCGACGGTATC 678

Db 1 TCGAGGTCGACGGTATC 17

RESULT 15

US-09-855-999-15
; Sequence 15, Application US/09855999
; Patent No. US20020119456A1
; GENERAL INFORMATION:
; APPLICANT: Van Ness, Jeffrey
; Tabone, John C.
; Howbert, J. Jeffrey

Mulligan, John T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETERMINING
; THE SEQUENCE OF NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED INTELLECTUAL PROPERTY LAW GROUP PLLC
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/855,999
; FILING DATE: 14-May-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David W.
; REGISTRATION NUMBER: 37,414
; REFERENCE/DOCKET NUMBER: 780068.416C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-855-999-15
Query Match 1.1%; Score 17; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 662 TCGAGGTCGACGGTATC 678
Db 1 TCGAGGTCGACGGTATC 17
Search completed: December 14, 2002, 08:34:43
Job time : 720 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 14, 2002, 06:56:12 ; Search time 26 Seconds
(without alignments)
796.026 Million cell updates/sec

Title: US-09-786-960-2

Perfect score: 2669

Sequence: 1 AIGPVASLVWANAPVSPDGF.....VPKAWSDLCPYDGLSEANQ 499

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2662	99.7	519	1	LAC2_TRAVE
2	2656	99.5	519	1	LAC2_TRAVI
3	2643	84.0	520	1	LAC1_CORHI
4	2194	82.2	520	1	LAC1_TRAVI
5	1917.5	71.8	527	1	LAC5_TRAVI
6	1916.5	71.8	527	1	LAC5_TRAVE
7	1882.5	70.5	520	1	LAC4_TRAVE
8	1871.5	70.1	520	1	LAC4_TRAVI
9	1743.5	65.3	529	1	LAC1_PLEOS
10	1743.5	65.3	533	1	LAC2_PLEOS
11	1716	64.3	548	1	LAC1_PHLRA
12	1606.5	60.2	473	1	LAC3_TRAVI
13	1219.5	45.7	520	1	LAC2_AGABI
14	1192.5	44.7	520	1	LAC1_AGABI
15	1077	40.4	531	1	LAC4_THACU
16	992	37.2	599	1	LAC2_THACU
17	930.5	34.9	572	1	LAC3_THACU
18	901	33.8	576	1	LAC1_THACU
19	622.5	23.3	621	1	LAC2_PODAN
20	614.5	23.0	624	1	FET3_CANAL
21	607.5	22.8	591	1	LAC1_CRYPA
22	601.5	22.5	619	1	LAC1_NEUCR
23	600.5	22.5	619	1	LAC2_NEUCR
24	599	22.4	636	1	FET3_YEAST
25	597.5	22.4	622	1	FET5_YEAST
26	583.5	21.9	486	1	LAC1_BOTCI
27	556	20.8	622	1	YAK8_SCHPO
28	536.5	20.1	587	1	ASO_CUCSA
29	530.5	19.9	578	1	ASO_TOBAC
30	510	19.1	552	1	ASO_CUCPM
31	501	18.8	579	1	ASO_CUCMA
32	392	14.7	608	1	YD56_YEAST
33	333	12.5	609	1	LAC1_EMENI

ALIGNMENTS

RESULT 1

ID	LAC2_TRAVE	STANDARD;	PRT;	519 AA.
AC	Q12718: Q12716;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Laccase 2 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)			
DE	(Urishiol oxidase) (Diphenol oxidase) (Laccase I).			
GN	LCC2 OR LCCI			
OS	Trametes versicolor (White-rot fungus).			
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC	Aphyllophorales; Trametes.			
OX	NCBI_TaxID=5325;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=52J;			
RX	MEDLINE=97464057; PubMed=9322748;			
RA	Er A., Pollock W.B., Smith M.;			
RT	"Cloning and sequence analysis of two laccase complementary DNAs from the ligninolytic basidiomycete Trametes versicolor.";			
RL	Gene 196:113-119(1997).			
CC	- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED PRODUCTS (PROBABLE).			
CC	- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzoquinone + 2 H(2)O.			
CC	- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.			
CC	- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U44851; AAA86659.1; -			
DR	EMBL: U44430; AAC49828.1; -			
DR	HSSP: F37064; IAC02.			
DR	InterPro: IPR001117; Cu-oxidase.			
DR	InterPro: IPR002355; MultiCu_oxidase2.			
DR	Pfam: PF00394; Cu-oxidase; 3.			
DR	PROSITE: PS00079; MULTICOPPER_OXIDASE1.			
DR	PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.			
KW	Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;			
KW	Lignin degradation; Multigene family.			
FT	SIGNAL 1 20			
FT	CHAIN 21 519			
FT	DOMAIN 22 147			
FT	DOMAIN 159 301			
FT	DOMAIN 368 490			

34	272	10.2	555	1	ASO_BRANA	Q00624	brassica na
35	271.5	10.2	605	1	PCOA_ECOLI	Q47452	escherichia
36	270.5	10.1	609	1	COPA_PESM	P12374	pseudomonas
37	266	10.0	554	1	NTP3_TOBAC	P29162	nicotiana t
38	207	7.8	572	1	BLRO_MYRVE	Q12737	myrothecium
39	173.5	6.5	513	1	COTA_BACSU	P07788	bacillus su
40	166.5	6.2	516	1	CUEO_ECOLI	P36649	escherichia
41	164.5	6.2	516	1	CUEO_ECO57	Q8X947	escherichia
42	155.5	5.8	533	1	CUEO_YERPE	Q82BK0	yersinia pe
43	138.5	5.2	536	1	CUEO_SALTI	Q829E1	salmonella
44	138.5	5.2	536	1	CUEO_SALTY	Q8ZRS2	salmonella
45	126	4.7	470	1	SUFI_ECOLI	P26648	escherichia

```
FT METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 418 418 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 420 420 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 472 472 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 69 69 D -> V (IN REF. 1: AAC49828).
SQ SEQUENCE 519 AA; 55810 MW; BFFB5B4CD0007702 CRC64;

Query Match 99.7%; Score 2662; DB 1; Length 519;
Best Local Similarity 99.8%; Pred. No. 8.2e-183;
Matches 498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AIGPVASLVANAVSPDGFRLDAIVNGVVPSPDLITCKGDRQLNVVDLTNHSMLKS 60
Db 21 AIGPVASLVANAVSPDGFRLDAIVNGVVPSPDLITCKGDRQLNVVDLTNHSMLKS 80
Qy 61 TSIHWHGFFOAGTNWADGPAFVNQCPTASGHSFLYDFHVPDQAGTFWVHSLSTQYCDGL 120
Db 81 TSIHWHGFFOAGTNWADGPAFVNQCPTASGHSFLYDFHVPDQAGTFWVHSLSTQYCDGL 140
Qy 121 RGPFFVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPFPFLGADATLNGLSRST 180
Db 141 RGPFFVYDPKPHASRYDNDNESTVITLTDWYHTAARLGPFPFLGADATLNGLSRST 200
Qy 181 PTAALAVINVOHGKRYRFLYSISCDPNYTFSDIGNLTVEVDGINSQPLLVDSIQIFA 240
Db 201 PTAALAVINVOHGKRYRFLYSISCDPNYTFSDIGNLTVEVDGINSQPLLVDSIQIFA 260
Qy 241 AQRYSFVLNANOTGVNWRANPNFTGVGFAGGINSALTRYQGPAPVABPTTTQTTSTVPL 300
Db 261 AQRYSFVLNANOTGVNWRANPNFTGVGFAGGINSALTRYQGPAPVABPTTTQTTSTVPL 320
Qy 301 IETNLHPLARMPVPGSPPTGGVDKALNLAENFNGTNEFFINNATFTPTVPVLLQTLGSAQ 360
Db 321 IETNLHPLARMPVPGSPPTGGVDKALNLAENFNGTNEFFINNATFTPTVPVLLQTLGSAQ 380
Qy 361 TAQDLLPAGSVYPLPAHSTIETLPATAPAGPFPFLHGHAFVAVRSAGSTTYNYNDP 420
Db 381 TAQDLLPAGSVYPLPAHSTIETLPATAPAGPFPFLHGHAFVAVRSAGSTTYNYNDP 440
Qy 421 IFRDVSVTGTGAAGDNVTIRFQTDNPGPWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVSVTGTGAAGDNVTIRFQTDNPGPWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 500
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 501 PKAWSDLCPYDGLSEANQ 519

RESULT 2
LAC2_TRAVI
ID LAC2_TRAVI STANDARD; PRT; 519 AA.
AC Q99046;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (dipheno oxidase).
```

```
GN LCC2.
OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OX Aphyllophorales; Trametes.
RN NCBI_TaxID=47662;
RP [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Mycelium;
RC MEDLINE=97076915; PubMed=8975613;
RA Yaver D.S., Xu F., Golightly E.J., Brown K.M., Brown S.H.,
RA Rey M.W., Schneider P., Halkier T., Mondorf K., Dalboge H.;
RT "Purification, characterization, molecular cloning, and expression of
RT two laccase genes from the white rot basidiomycete Trametes
RT villosa.";
RL Appl. Environ. Microbiol. 62:834-841(1996).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L49377; AAC41687.1; -.
DR HSP; P37064; LAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 519 LACCASE 2.
FT DOMAIN 22 147 PLASTOCYANIN-LIKE 1.
FT DOMAIN 159 301 PLASTOCYANIN-LIKE 2.
FT DOMAIN 368 490 PLASTOCYANIN-LIKE 3.
FT METAL 84 84 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 86 86 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 131 131 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 415 415 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 418 418 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 420 420 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 472 472 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 474 474 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 478 478 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 519 AA; 55777 MW; DBB4EA526F684740 CRC64;

Query Match 99.5%; Score 2656; DB 1; Length 519;
Best Local Similarity 99.4%; Pred. No. 2.2e-182;
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Matches 456; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AIGPVASLVVANAPSPDGLRDAIVVGVVPSPLITGKGGDRFQNLNVVDVTLNHSMLKS 60
Db 21 AIGPVASLVVANAPSPDGLRDAIVVGVVPSPLITGKGGDRFQNLNVVDVTLNHSMLKS 80
QY 61 TSHHWGFFQAGTNWADGPAFVNOCPISAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
Db 81 TSHHWGFFQAGTNWADGPAFVNOCPISAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 140
QY 121 RGFVVYDPRKHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLNGLSRST 180
Db 141 RGFVVYDPRKHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLNGLSRST 200
QY 181 PTAALAVINVQHGKRYRFRFLVLSISCDPNYTFSDIGHNLTVIEVDGINSQPLLVDSIQIFA 240
Db 201 PTAALAVINVQHGKRYRFRFLVLSISCDPNYTFSDIGHNLTVIEVDGINSQPLLVDSIQIFA 260
QY 241 AQYSFVLNANQTVGNVWRANPNFTGVFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
Db 261 AQYSFVLNANQTVGNVWRANPNFTGVFAGGINSAILRYOGAPVAEPTTTQTSVIPL 320
QY 301 IETNLHPLARMVPVPGSPGTGGVDKALNLAFFNENGTFFINNAFTPTPTVPLQLIISGAQ 360
Db 321 IETNLHPLARMVPVPGSPGTGGVDKALNLAFFNENGTFFINNAFTPTPTVPLQLIISGAQ 380
QY 361 TAQDLPLAGSVYPLPAHSTIETLPTALAPAGPAPHPFLHGHAFVAVRSAGSTTYNNDP 420
Db 381 TAQDLPLAGSVYPLPAHSTIETLPTALAPAGPAPHPFLHGHAFVAVRSAGSTTYNNDP 440
QY 421 IFRDVTSTGTPAAGDNTVTRFQDNPWPFLHCHIDFHLDAFPAIYFAEDVADVKAANPV 480
Db 441 IFRDVTSTGTPAAGDNTVTRFQDNPWPFLHCHIDFHLDAFPAIYFAEDVADVKAANPV 500
QY 481 PRAWSDLCPYDGLSEANQ 499
Db 501 PRAWSDLCPYDGLSEANQ 519

RESULT 3
LAC1CORHI
ID LAC1CORHI STANDARD; PRT; 520 AA.
AC Q02497;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Laccase precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Ligninolytic phenoloxidase).
OS Coriolus hirsutus.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Coriolus.
ON NCBI_TaxID=5327;
RX STRAIN=IFO 4917;
RX MEDLINE=90368706; PubMed=2394718;
RA Kojima Y., Tsukuda Y., Kawai Y., Tsukamoto A., Sugura J.,
RA Sakano M., Kita Y.
RT "Cloning, sequence analysis, and expression of ligninolytic
RT phenoloxidase genes of the white-rot basidiomycete Coriolus
RT hirsutus."
RL J. Biol. Chem. 265:15224-15230(1990).
CC -1- FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT ROLE IN LIGNIN
CC DEGRADATION. CLEAVES THE C-C AND C-O BONDS OF SOME PHENOLIC LIGNIN
CC MODEL COMPOUNDS (SUCH AS O- AND P-QUINOLS, AMINOPHENOLS AND
CC PHENYLENEDIAMINE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenesemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- POLYMORPHISM: 2 ALLELIC FORMS VARYING IN ONE AA POSITION.
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CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC
CC EMBL; M60560: AAA33103.1; -
CC EMBL; M60561: AAA33104.1; -
CC PIR; A35883; A35883.
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; MultiCu_oxidase2.
CC Pfam; PF00394; Cu-oxidase; 3.
CC PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
CC PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
CC Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
CC Glycoprotein; Repeat.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 520 LACCASE.
CC DOMAIN 23 148 PLASTOCYANIN-LIKE 1.
CC DOMAIN 160 302 PLASTOCYANIN-LIKE 2.
CC DOMAIN 369 491 PLASTOCYANIN-LIKE 3.
CC METAL 85 85 COPPER (TYPE 2) (BY SIMILARITY).
CC METAL 87 87 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 132 132 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 416 416 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 419 419 COPPER (TYPE 2) (BY SIMILARITY).
CC METAL 421 421 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 474 474 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL 475 475 COPPER (TYPE 3) (BY SIMILARITY).
CC METAL 479 479 COPPER (TYPE 1) (BY SIMILARITY).
CC METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
CC CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 229 229 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
CC DISULFID 106 509 POTENTIAL.
CC DISULFID 138 226 POTENTIAL.
CC VARIANT 411 411 A -> P.
CC CONFLICT 378 379 SG -> RR (IN REF. 1; AAA33104).
CC SEQUENCE 520 AA; 55688 MW; 977D8DFA551F7929 CRC64;

Query Match 84.0%; Score 2243; DB 1; Length 520;
Best Local Similarity 81.8%; Pred. No. 6.7e-153;
Matches 408; Conservative 35; Mismatches 56; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPSPDGLRDAIVVGVVPSPLITGKGGDRFQNLNVVDVTLNHSMLKS 60
Db 22 AIGPTADLTISNAEVSPPDGFARQAVVNVNTPGLVAGNKGDRFQNLNVIDLNTHTMLKS 81
QY 61 TSHHWGFFQAGTNWADGPAFVNOCPISAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
Db 82 TSHHWGFFQAGTNWADGPAFVNOCPISAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 141
QY 121 RGFVVYDPRKHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLNGLSRST 180
Db 142 RGFVVYDPRKHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLNGLSRST 201
QY 181 PTAALAVINVQHGKRYRFRFLVLSISCDPNYTFSDIGHNLTVIEVDGINSQPLLVDSIQIFA 240
Db 202 TAADLAVINVTKGKRYRFRFLVLSISCDPNYTFSDIGHNLTVIEVDGINSQPLLVDSIQIFA 261
QY 241 AQYSFVLNANQTVGNVWRANPNFTGVFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
```

Db 262 AQRYSVFLNADQDVGNVWIRANPNFGNYGAGGINSAILRYDGDVPEPTTQTTPKPL 321
QY 301 IETNLHPLARMPVPGSPGVDKALNLAFFNFGNTEFNINATETPTVPVLLQILSGAQ 360
Db 322 NEVDLHPLATMAVPGSPVAGGVDTATNMAFNFGNFTINGASFVPTVPVLLQILSGAQ 381
QY 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLGHAFVAVRSAGSTTYNDP 420
Db 382 NAQDLLPAGSVYSLPSNADIEISFPATAAPGAPHPFHLGHAFVAVRSAGSTTYNDP 441
QY 421 IFRDVSSTGTPAAGDNVTIRFOTDNPFGWFLHCHIDFHLDAAGFAIVFAEDVADYKAANPV 480
Db 442 IFRDVSSTGTPAAGDNVTIRFOTDNPFGWFLHCHIDFHLDAAGFAIVFAEDIPDVASANPV 501
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 502 QAWSDLCPYDALDVNDQ 520

RESULT 4
LAC1_TRAVI
ID LAC1_TRAVI STANDARD; PRT; 520 AA.
AC Q99044;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Laccase 1 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCCL

OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
ON NCBI_TaxID=47662;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mycelium;
RX MEDLINE=97076915; PubMed=9975613;
RA Yaver D.S., Xu F., Golightly E.J., Brown K.M., Brown S.H.,
RA Rey M.W., Schneider P., Halkier T., Mondorf K., Balboe H.;
RT "Purification, characterization, molecular cloning, and expression of
RT two laccase genes from the white rot basidiomycete Trametes
RT villosa".
RL Appl. Environ. Microbiol. 62:834-841(1996).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.

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EMBL; L49376; AAC41686.1; -
DR HSSP; P37064; 1A0Z.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
DR Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family.
FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 520
FT DOMAIN 23 148
FT DOMAIN 160 302
FT DOMAIN 369 491
FT METAL 85 85
FT METAL 87 87
FT METAL 130 130
FT METAL 132 132
FT METAL 416 416
FT METAL 419 419
FT METAL 421 421
FT METAL 473 473
FT METAL 474 474
FT METAL 475 475
FT METAL 479 479
FT METAL ?
FT CARBOHYD 72 72
FT CARBOHYD 75 75
FT CARBOHYD 229 229
FT CARBOHYD 238 238
FT CARBOHYD 354 354
FT CARBOHYD 361 361
FT CARBOHYD 457 457
SQ SEQUENCE 520 AA; 55545 MW; 046AB6D74737C60E CRC64;

Query Match 82.2%; Score 2194; DB 1; Length 520;
Best Local Similarity 79.7%; Pred. No. 2.1e-149;
Matches 397; Conservative 36; Mismatches 65; Indels 0; Gaps 0;

Qy 2 IGPVASLVANAPVSPDGLFRDAIVVNGVPSPLITGKKGDRFQNLNVVDTLTNHSMLKST 61
Db 23 IGPVADLTITNAAVSPDGFGRQAVVNGTGPGLITKMGDRFQNLNVDTLTNHSMLKST 82
QY 62 SIHWHGFFQAGTNWADGPAFYNQCPISGSHSLYDFYVDDQAGTFWYHSHLSTQYCDGLR 121
Db 83 SIHWHGFFQAGTNWADGPAFYNQCPISGSHSLYDFYVDDQAGTFWYHSHLSTQYCDGLR 142
QY 122 GPFVYVDPKPHASRYVDVNESTVITLTDWYHTAARGLRFPPLGADATLNLGLRSASTP 181
Db 143 GPFVYVDPNDPAADLYDVNDNDTIVITLVDWYHVAAGLPAFLGADATLNLGLRSASTP 202
QY 182 TAALAVINQHGKRYRFRFLVSIQCDPNYTFSDIGNHLTVIEVDGINSOPLLVDSIQIFAA 241
Db 203 TADLSVSTVTPKRYRFRFLVSLQCDPNYTFSDIGNHMTIETDSINTAPLVDSIQIFAA 262
QY 242 QRYSFVLNANQTVGNVWRANPNFTGTFAGGINSAILRYOCAPVAEPTTQTTSVIPLI 301
Db 263 QRYSFVLEANAQVDNYWIRANPNFGNVTGGINSAIRLYDGAAGVEPTTQTTSVIPLI 322
QY 302 ETNLHPLARMPVPGSPGVDKALNLAFFNFGNTEFNINATETPTVPVLLQILSGAQ 361
Db 323 EVNLHPLVTTAVPGSPVAGGVDTATNMAFNFGNFTINGASFVPTVPVLLQILSGAQ 382
QY 362 AQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLGHAFVAVRSAGSTTYNDP 421
Db 383 AQDLLPAGSVYSLPSNADIEISFPATAAPGAPHPFHLGHAFVAVRSAGSTTYNDP 442
QY 422 IFRDVSSTGTPAAGDNVTIRFOTDNPFGWFLHCHIDFHLDAAGFAIVFAEDVADYKAANPV 481
Db 443 IFRDVSSTGTPAAGDNVTIRFOTDNPFGWFLHCHIDFHLDAAGFAIVFAEDIPDVASANPV 502
QY 482 KAWSDLCPYDGLSEANQ 499
Db 503 QAWSDLCPYDALDVNDQ 520

RESULT 5
LAC5_TRAVI
ID LAC5_TRAVI STANDARD; PRT; 527 AA.
AC Q99056;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Laccase 5 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
 DE (Urishiol oxidase).
 GN LC5.
 OS Trametes villosa (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 OX NCBI_TaxID=47662;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97128774; PubMed=8973314;
 RA Yaver D.S., Gollightly E.J.;
 RT "Cloning and characterization of three laccase genes from the
 RT white-rot basidiomycete Trametes villosa: genomic organization of the
 RT laccase gene family.";
 RL Gene 181:95-102(1996).
 RN [2]
 RP REVISIONS.
 RA Yaver D.S., Gollightly E.J.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
 CC PRODUCTS (PROBABLE).
 CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenediol + 2
 CC H(2)O.
 CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
 CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
 CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC -----
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 DR EMBL; L78078; AB47735.2; -.
 DR HSSP; P37064; IAOZ.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR002355; MultiCu_oxidase2.
 DR Pfam; PF00394; Cu-oxidase; 3
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
 DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; FALSE_NEG.
 KW Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
 KW Lignin degradation; Multigene family.
 FT SIGNAL 1 23
 FT CHAIN 24 527
 FT LACCASE 5.
 FT DOMAIN 25 150
 FT PLASTOCYANIN-LIKE 1.
 FT DOMAIN 162 306
 FT PLASTOCYANIN-LIKE 2.
 FT DOMAIN 373 498
 FT PLASTOCYANIN-LIKE 3.
 FT METAL 87 87
 FT COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 89 89
 FT COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 132 132
 FT COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 134 134
 FT COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 425 425
 FT COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 428 428
 FT COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 430 430
 FT COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 480 480
 FT COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 481 481
 FT COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 482 482
 FT COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 486 486
 FT COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL ? ?
 FT COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 74 74
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 77 77
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT METAL 156 156
 FT COPPER (TYPE 3) (BY SIMILARITY).
 FT CARBOHYD 209 209
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT METAL 233 233
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 242 242
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT METAL 276 276
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 317 317
 FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 358 358 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 527 AA; 56247 MW; F1BE638D5FFA478 CRC64;
 Query Match 71.8%; Score 1917.5; DB 1; Length 527;
 Best Local Similarity 70.5%; Pred. No. 1.2e-129;
 Matches 356; Conservative 47; Mismatches 93; Indels 9; Gaps 3;
 QY 1 AIGPVASLVVANAPVSPDGFRLDAIVVNGVPSPLITGKKGRFQINNVVDITNNHSLKLS 60
 DB 24 AIGPVTDLTISNADYTPDGIITRAAVALAGGVFPGLITGKNGDEFOINVINDLNTNETMLKS 83
 QY 61 TSIHWHGFQAGTINWADGPAFVNOCPAGSHSFLVDFHVPDQAGTFWYHSHLSYQCDGL 120
 DB 84 TTIHWHGIFQAGTINWADGPAFVNOCPAGSHSFLVDFHVPDQAGTFWYHSHLSYQCDGL 143
 QY 121 RGFVVYDPKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATFLINGLGRSAST 180
 DB 144 RGPLVVYDPDDPNASLYDVEDDTTITLADWYHTAARLGRPFPLGADATFLINGLGRSAST 203
 QY 181 PTAA--LAVINVQHKRYRFRFLVSISCDPNYTFSDGHNLTVEVDGINSQPLLYVDSIOI 238
 DB 204 GGGATNLTVITVTOGKRYRFRFLVSISCDPNYTFSDGHNLTVEVDGINSQPLLYVDSIOI 263
 QY 239 FAAQYSYFVLNANQTVGNVWVRANFNGVFGAGGINSAILRYOGAPVAPPTTOTTTSVI 298
 DB 264 FAGQYSYFVLNANQTVGNVWVRANFNGVFGAGGINSAILRYOGAPVAPPTTOTTTSVI 323
 QY 299 PLIETNLHPLAMPVPGSTPGGVKALNLFNFGTNNFNNATFTPTPVLLQILSG 358
 DB 324 PLUTETDLVPLNDPAAPGDPQGVGVDLAMSLDFSNFNNFNNATFTPTPVLLQILSG 383
 QY 359 ACTAODLLPAGSVPLPAHSTIEITLPATAL-----AGCAPHFLHGHAFVVSAGST 413
 DB 384 ADAASLPLNGSVYITLPSNSTIEISPIITTDGVLNAPGAPHPFLHGHFTFSVRSAGSS 443
 QY 414 TYNNDPIFRDVTSTGTPAAGDNVTIRFQDTPNGPFWLHCHIDFHLDAAGFAIVFEDVAD 473
 DB 444 TFNYANPYRRDVTSTG--SGDNVTIRFQDTPNGPFWLHCHIDFHLDAAGFAIVFEDVAD 501
 QY 474 VKAANPVKANSDLCPIDVGLSEAN 498
 DB 502 TASANPVFTANSDLCPITYDALDSSD 526
 RESULT 6
 LAC5_TRAVE STANDARD: PRT; 527 AA.
 ID LAC5_TRAVE
 AC Q12717;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Laccase 5 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
 DE (Urishiol oxidase) (Diphenol oxidase) (Laccase IV).
 GN LC5 OR LCIV.
 OS Trametes versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 OX NCBI_TaxID=5325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=52J;
 RX MEDLINE=97464057; PubMed=9322748;
 RA Ong E., Pollock W.B., Smith M.;
 RT "Cloning and sequence analysis of two laccase complementary DNAs from
 RT the ligninolytic basidiomycete Trametes versicolor.";
 RL Gene 196:113-119(1997)
 CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
 CC PRODUCTS (PROBABLE).
 CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenediol + 2

DR	PROSITE: P500080; MULTICOPPER_OXIDASE2; FALSE_NEG.	
KW	Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;	
KW	Lignin degradation; Multigene family.	
FT	SIGNAL 1 22	POTENTIAL.
FT	CHAIN 23 520	LACCASE 4.
FT	DOMAIN 24 149	PLASTOCYANIN-LIKE 1.
FT	DOMAIN 161 303	PLASTOCYANIN-LIKE 2.
FT	DOMAIN 370 491	PLASTOCYANIN-LIKE 3.
FT	DISULFID 107 509	PROBABLE.
FT	DISULFID 139 227	PROBABLE.
FT	METAL 86 86	COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL 88 88	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 131 131	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 133 133	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 418 418	COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL 421 421	COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL 423 423	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 473 473	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 474 474	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 475 475	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 479 479	COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL ? ?	COPPER (TYPE 1) (BY SIMILARITY).
FT	CARBOHYD 73 73	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 76 76	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 239 239	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 399 399	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 457 457	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 497 497	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE 520 AA; 55643 MW; FC1032400E9DDFA4 CRC64;	
Query Match 70.5%; Score 1882.5; DB 1; Length 520;		
Best Local Similarity 69.1%; Pred. No. 3.6e-127;		
Matches 345; Conservative 56; Mismatches 95; Indels 3; Gaps 2;		
QY	1 AIGPVASLVVAVPSPDGLRDAIVVGVPSPLITGKGRFQNLNVVDVTLNHSMLKS 60	
DB	23 AIGPVTDLTISNADSPDGFTRAAVLANGVFPCPLITGKGNQFNQINDLSNETMLKS 82	
QY	61 TSHHGHGFQAGTNWADGPAFNQCPDIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120	
DB	83 TSHHGHGFQKGNWADGAAFNQCPDIATGNSFLYDFATDQAGTFWYHSHLSTQYCDGL 142	
QY	121 RGPVYVDKPDHASYDYVDNESTVTLTDVHTAARLGRPRPLGADATLNGLSRST 180	
DB	143 RGPVYVDSPDHPADLYDVEDTITLSDVHTAASLGAAFPDGSFSLINGLGRFAGG 202	
QY	181 PTAALAVINVQHGKRYRFLVLSICDPNTYFSDGHNLTVIEVDGINSQPLLVDSIQIFA 240	
DB	203 DSTDLAVITVEQGRYMRLLSLSCPNYVFSIDGHNMVTIEADAVNHEPLTVDSIQIVA 262	
QY	241 AQRYSEVLNANTVGNVWRANPNFCTGVFAGGINSAILRYQCAPVAEPTTTQTSVIPL 300	
DB	263 GQRYSEVLADQDIDNIFYRALPSAGTTSFDDGINSAILRYSGASEVDPTTTTTSVLPL 322	
QY	301 IETNLHPLARMVPVPGSPTPGVDKALNLFNNGTFFNNAFTPTPTVPVLQILSGAQ 360	
DB	323 DEANVPLDSPRAPGPNIGVDYALNLDNFEDGTFNFDVSVFPTVPVLQILSGTT 382	
QY	361 TAODLLPAGSVPLPAHSTIETLPTAL-APGAPHPFLHGHAFVAVRSAGSTTYNYND 419	
DB	383 SAADLLPSGLFALPSNSTIEISFPITATNAPGAPHPFLHGHGTFIVRTAGSTDNEVN 442	
QY	420 PFRDVSVGTGTAAGDNVIRQTQDNPNGPWFHLCHDFHLDAGFAIVFADVADVKAAP 479	
DB	443 PVHRDVVNTGT--AGDNVIRFTDNPNGPWFHLCHDFHLEAGFAIVFSDADVSNNTT 500	
QY	480 VPKAWSDLCPIDYGLSEAN 498	
DB	501 PSTAWEDLCPTYNALDSSD 519	
RESULT 8		
LAC4_TRAVI		

ID	LAC4_TRAVI	STANDARD;	PRT;	520 AA.
AC	Q99055;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Laccase 4 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)			
GN	(Urishiol oxidase) (Diphenol oxidase).			
OS	LCC4.			
OS	Trametes villosa (White-rot fungus).			
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;			
OC	Aphyllophorales; Trametes.			
OX	NCBI_TaxID=47662;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97128774; PubMed=8973314;			
RA	Yaver D.S., Golightly E.J.;			
RT	"Cloning and characterization of three laccase genes from the			
RT	white-rot basidiomycete Trametes villosa: genomic organization of the			
RT	laccase gene family.";			
RL	Gene 181:95-102(1996).			
CC	-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED			
CC	PRODUCTS (PROBABLE).			
CC	-!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2			
CC	H(2)O.			
CC	-!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU			
CC	CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE			
CC	3 OR COUPLED BINUCLEAR (BY SIMILARITY).			
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.			
CC	-!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; L78077; AAB47734.1; -.			
DR	HSP; P37064; IASO.			
DR	InterPro: IPR001117; Cu-oxidase.			
DR	InterPro: IPR002355; MultiCu_oxidase2.			
DR	Protein: P500080; Cu-oxidase; 3.			
DR	PROSITE: P500079; MULTICOPPER_OXIDASE1; 1.			
DR	PROSITE: P500080; MULTICOPPER_OXIDASE2; FALSE_NEG.			
KW	Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;			
KW	Lignin degradation; Multigene family.			
FT	SIGNAL 1 18	POTENTIAL.		
FT	CHAIN 19 520	LACCASE 4.		
FT	DOMAIN 24 149	PLASTOCYANIN-LIKE 1.		
FT	DOMAIN 161 303	PLASTOCYANIN-LIKE 2.		
FT	DOMAIN 370 491	PLASTOCYANIN-LIKE 3.		
FT	METAL 86 86	COPPER (TYPE 2) (BY SIMILARITY).		
FT	METAL 88 88	COPPER (TYPE 3) (BY SIMILARITY).		
FT	METAL 131 131	COPPER (TYPE 3) (BY SIMILARITY).		
FT	METAL 133 133	COPPER (TYPE 3) (BY SIMILARITY).		
FT	METAL 418 418	COPPER (TYPE 1) (BY SIMILARITY).		
FT	METAL 421 421	COPPER (TYPE 2) (BY SIMILARITY).		
FT	METAL 423 423	COPPER (TYPE 3) (BY SIMILARITY).		
FT	METAL 473 473	COPPER (TYPE 3) (BY SIMILARITY).		
FT	METAL 474 474	COPPER (TYPE 1) (BY SIMILARITY).		
FT	METAL 475 475	COPPER (TYPE 3) (BY SIMILARITY).		
FT	METAL 479 479	COPPER (TYPE 1) (BY SIMILARITY).		
FT	METAL ? ?	COPPER (TYPE 1) (BY SIMILARITY).		
FT	CARBOHYD 73 73	N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 76 76	N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 239 239	N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 399 399	N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 457 457	N-LINKED (GLCNAC. .) (POTENTIAL).		
FT	CARBOHYD 497 497	N-LINKED (GLCNAC. .) (POTENTIAL).		
SQ	SEQUENCE 520 AA; 55643 MW; 16469DC547C61F3C CRC64;			

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Query Match 70.1%; Score 1871.5; DB 1; Length 520;
Best Local Similarity 68.5%; Pred. No. 2.2e-126;
Matches 342; Conservative 57; Mismatches 97; Indels 3; Gaps 2;

Qy 1 AIGPVASLVANAPVSPDGFURDAIVNGVVPSPILITGKGRFQNLNVVDVTLTHSMKLS 60
Dy 23 AIGPVTLTISGVDVSPDGFTRAAVLAVNGVVPSPILITGKGRFQNLNVVDVTLTHSMKLS 82
Qy 61 TSIHWHGFQAGTNWAGPAFVNCPTASGHSFELYDEHVPDQAGTFWYHSHLSQYCDGL 120
Dy 83 TSIHWHGFQAGTNWAGPAFVNCPTASGHSFELYDEHVPDQAGTFWYHSHLSQYCDGL 142
Qy 121 RGFVFWYDPKPHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLNGLSRST 180
Dy 143 RGFVFWYDPKPHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLNGLSRST 202
Qy 181 PTAALAVINVOHGKRYRFLVSIISCDPNYFSDIGNHLTVTEVDGINSQPLLVDSIQIFA 240
Dy 203 DSTDLAVITVEQGRYRMRLLSLSCDPNYFSDIGNHLTVTEVDGINSQPLLVDSIQIFA 262
Qy 241 AQRSEVLNANOTGVNVRANPNFCVGFAGGINSAILRYQGPAPVAEPTTQTSVIPL 300
Dy 263 GQRYSEVLNANOTGVNVRANPNFCVGFAGGINSAILRYQGPAPVAEPTTQTSVIPL 322
Qy 301 IETNLHPLARMPVPGSPGGVDKALNLAFFNGFNFINNATFTPTVPVLLQILSGAQ 360
Dy 323 DEANLVPLDSPAAQDPNIGGVYDALNLDNFNCTGFINDVSEFVPIVLLQILSGQT 382
Qy 361 TAQDLFPAGSVYPLPAHSTIETITLPAATL-APGAPHPFLHGHAFVAVRSAGSTYNYND 419
Dy 383 SAADLLPSGSLFAVPSNTEISFIPATNAPGAPHPFLHGHAFVAVRSAGSTYNYND 442
Qy 420 PIERDVTSTGPAAGDNVTIFQDNDGCPWFLHCHIDPHLDAGFAIPEADVADKAMP 479
Dy 443 PVRDVTSTGPAAGDNVTIFQDNDGCPWFLHCHIDPHLDAGFAIPEADVADKAMP 500
Qy 480 VPKASDLCPIYDGLSEAN 498
Dy 501 PSTAWEDLCPIYALDSSD 519

RESULT 9
LACI_PLEOS STANDARD; PRT; 529 AA.
AC LACI_PLEOS
AD Q12729;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Laccase 1 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN POX1.
OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=5322;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida; TISSUE=Mycelium;
RX MEDLINE=95314294; PubMed=7793961;
RA Giardina P., Canio R., Martirani L., Marzullo L., Palmieri G.,
RA Sanna G.;
RT "Cloning and sequencing of a laccase gene from the lignin-degrading
RT basidiomycete Pleurotus ostreatus."
RL Appl. Environ. Microbiol. 61:2408-2413(1995).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLY).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
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Db 382 PVLLQLSGATTAALLPSGSIYSEANKVWEISIP--ALAVGGPHFPHLGHGTFDVIKS 439
Qy 410 AGSTTYNYNDPIFRDVTGGTGAAGGNTIRFOTONPGWFLHCHIDFHLDAAGFAIVPAE 469
Db 440 AGSTTYNEDTPARRDVTGGTGD-ANDNTYIRVTNPGWFLHCHIDHWHLEIGLAVVPAE 498
Qy 470 DVADVKAANPVKAWSLCPIYDGLSEANQ 499
Db 499 DVTSITAP---PAAWDDLCPYDALSDSDK 525

RESULT 10
LAC2_PLEOS STANDARD: PRT; 533 AA.
AC Q12739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Laccase 2 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (diphenol oxidase).
GN POX2.
OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=5322;
RN [1]
RP SEQUENCE FROM N. A., CARBOHYDRATE-LINKAGE SITE, AND MASS SPECTROMETRY.
RC TISSUE=Mycelium;
RX MEDLINE=96184523; PubMed=8654395;
RA Giardina P., Aurilia V., Cannio R., Marzullo L., Amoresano A.,
RA Siciliano R., Pucci P., Sannia G.;
RA Cannio R., Sannia G.;
RT "Stability and activity of a phenol oxidase from the ligninolytic
RT fungus pleurotus ostreatus.";
RL Eur. J. Biochem. 235:508-515(1996).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Florida; TISSUE=Mycelium;
RX MEDLINE=93356991; PubMed=7763931;
RA Palmieri G., Giardina P., Marzullo L., Desiderio B., Nitti G.,
RA Cannio R., Sannia G.;
RT "Stability and activity of a phenol oxidase from the ligninolytic
RT fungus pleurotus ostreatus.";
RL Appl. Microbiol. Biotechnol. 39:632-636(1993).
CC -!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -!- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenemiquinone + 2
CC H(2)O.
CC -!- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: N-GLYCOSYLATED AT ASN-467 BY A HIGH-MANNOSE STRUCTURE WITH A
CC VARYING NUMBER OF MANNOSE RESIDUES. THERE EXIST NO FURTHER POST-
CC TRANSITIONAL MODIFICATION.
CC -!- MISCELLANEOUS: POX2 ISOZYME IS THE MOST ABUNDANT LACCASE OF
CC P. OSTREATUS UNDER VARIOUS GROWTH CONDITIONS.
CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -!- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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DR EMBL; 249075; CAA88895.1; -
DR EMBL; 234848; CAA84357.1; -
DR HSSP; P37064; LAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; Multicu_oxidse2.
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DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 533 LACCASE 2.
FT DOMAIN 25 171 PLASTOCYANIN-LIKE 1.
FT DOMAIN 173 336 PLASTOCYANIN-LIKE 2.
FT DOMAIN 382 501 PLASTOCYANIN-LIKE 3.
FT METAL 98 98 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 100 100 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 145 145 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 427 427 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 430 430 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 432 432 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 483 483 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 484 484 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 485 485 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 489 489 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 467 467 N-LINKED (GLCNAC... ) (HIGH MANNOSE).
SQ SEQUENCE 533 AA; 56766 MW; 7233C41D47E19AE6 CRC64;

Query Match 65.3%; Score 1743.5; DB 1; Length 533;
Best Local Similarity 64.8%; Pred. No. 3.le-117;
Matches 330; Conservative 49; Mismatches 109; Indels 21; Gaps 7;

Qy 1 AIGPVASIVVANAPVSPDGFRLDAIVVNGV-----VPSPLITCKKGDRLQNVV 49
Db 24 AIGPAGNIVIVNEDVSPDGFARSVAARSVPATDTPATASIPVLVQKNGDNFQNVV 83
Qy 50 DPLTNHSLKSTSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTFWH 109
Db 84 NOLSDTHLKTTSIHWHGFFQAGSSWADGPAFVTCQPVASGDSFLYFNVPDQAGTFWH 143
Qy 110 SHLSTQYCDGLRGPVYVDPKDPHASRYDVNDNESVITLTDWYHTAARLGRPRFLGADAT 169
Db 144 SHLSTQYCDGLRGPVYVDPKDPHASRYDVNDNESVITLTDWYHTAARLGRPRFLGADAT 202
Qy 170 LINGGRASSTPTAALAVINVOHGRYRFLVSCDPNYTFSIDGHNLTIVLEVDGINSQ 229
Db 203 LINGGRAGGTPALAIINVESNRRLVSMSCDPNFTFSIDGHSLLVLEADAVNV 262
Qy 230 PLVDSIQIFAQRYSFVLNANQTVGNVWRANPFGTVGFAGGINSAILRQGGAPVAP 289
Db 263 PITVDSIQIFAQRYSFVLNANQTVGNVWRANPFGTVGFAGGINSAILRQGGAPVAP 322
Qy 290 TTTQTSVPIETNLHPLARMPVPGSPGVDKALNLAFFNGTNP--FTNNATFTPP 347
Db 323 TTTSTST-PLLETNLVPLENPGAPGPPVPGGADINILAMAFDFTTFTELTINGVPFLPP 381
Qy 348 TVPVLQLLSGAOTADLLPAGSVYPLPAHSTIETLTPATALAPGAPHPHHLGHAFV 407
Db 382 TAPVLQLLSGAOTADLLPAGSVYPLPAHSTIETLTPATALAPGAPHPHHLGHAFV 439
Qy 408 RSAGSTTYNYNDPIFRDVTGGTGAAGGNTIRFOTONPGWFLHCHIDFHLDAAGFAIV 467
Db 440 RSAGSTTYNYNDPIFRDVTGGTGAAGGNTIRFOTONPGWFLHCHIDFHLDAAGFAIV 498
Qy 468 REDVADVKAANPVKAWSLCPIYDGLSE 496
Db 499 AEDVTSITAP---PAAWDDLCPYDALSD 524

RESULT 11
LAC1_PHLRA
ID LAC1_PHLRA STANDARD: PRT; 548 AA.
AC Q01679;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

DE Laccase precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
DE (Urishiol oxidase) (Ligninolytic phenoloxidase).
GN LAC.
OS Phlebia radiata (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Corticiaceae; Phlebia.
OX NCBI_TaxID=5308;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 6458;
RX MEDLINE=92065223; PubMed=1955850;
RA Saohelimo M., Niku-Paavola M.L., Knowles J.K.;
RT Isolation and structural analysis of the laccase gene from the
RT lignin-degrading fungus *Phlebia radiata*.;
RL J. Gen. Microbiol. 137:1537-1544(1991).
CC -1- FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT ROLE IN LIGNIN
CC DEGRADATION.
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; X52134; CAA36379.1; -;
DR EMBL; A20705; CAA01513.1; -;
DR PIR; S18746; S18746.
DR HSP; P37064; IASQ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat.
FT SIGNAL 1 21
FT CHAIN 22 548
FT DOMAIN 22 148
FT DOMAIN 160 304
FT DOMAIN 373 496
FT METAL 85 85
FT METAL 87 87
FT METAL 130 130
FT METAL 132 132
FT METAL 418 418
FT METAL 421 421
FT METAL 423 423
FT METAL 473 473
FT METAL 474 474
FT METAL 475 475
FT METAL 479 479
FT METAL 484 484
FT CARBOHYD 75 75
FT CARBOHYD 352 352
FT CARBOHYD 402 402
FT CARBOHYD 457 457
SQ SEQUENCE 548 AA; 58601 MW; 3445A757E3C56B2 CRC64;
Query Match 64.3%; Score 1716; DB 1; Length 548;
Best local similarity 69.4%; Pred. No. 3e-115;
Matches 326; Conservative 42; Mismatches 92; Indels 10; Gaps 6;
QY 1 AIGFVASLVVAPSPDGLRDAIVVGVPSFLITGKGRFQLNVVDTLNHSMLKS 60

Db 22 SIGPVTDFHVNAAVSPDGFSGQAVLAEGVFPGPLIAGNKGDNFQINVIDELTNATMLKT 81
QY 61 TSHHGHGFFOAGTNWADGPAFVNOCTASGHSFLYDFHVPDQAGTFWYHSHLSYQYCDGL 120
Db 82 TTHHGHGFFOAGTNWADGPAFVNOCTASGHSFLYDFHVPDQAGTFWYHSHLSYQYCDGL 141
QY 121 RGPVYVDPKDPHASRYDVNDNESTVITLTDMYHTAARLGRPFPLGADATLINGLGR--SA 178
Db 142 RGPVYVDPADPYLDQYDVDDSTVITLADYHTAARLGRSFPF-AADTTILINGLGRGEA 200
QY 179 STTAALAVINVQHKRYRFLVSLVSDPNYTFSDGHNLTVIEVDGINSQPLLVDSIQI 238
Db 201 GCPVSDLAIVSVTKRYRFLVSLVSDPSTFSDGHNLTVIEVDATNHPQLTVDELTI 260
QY 239 FAQRYSFVLNANQTVGNVYVRANPNFG-TVGAGGINSAILRYQGAPEPTTQTSV 297
Db 261 YAGORYSFILTAODVDVNIWRANPGIGITGAGGINSAILRYQGAPEPTTQTSV 320
QY 298 IPIETNLHPLARMPVPGSPTPGVDKALNAFNFNGTN--FFINNAFTPTTPVVLQI 355
Db 321 VVLSNLAFLPTNAAAPGLPEVGVDLALNFLTDFGSPSLKFOINGVTFVPTVPVLQI 380
QY 356 LSGAQTADLLPAGSVYPLPAHSTIETITPATALAPCAPHPHLHGHAFVAVRSAGTTY 415
Db 381 LSGAQAADLLPGSVYALPSNATIELSLPAGAL--GGPHPHLGHGTFVSVRPAGSTTY 438
QY 416 NYNDPFRDVTGTGTPAAGNVIRFQTDNPGPWFHLCHIDFHLDAAGAI 465
Db 439 NYNVPQDVVVSIGN--TGDNVIRDTNPNPGPWFHLCHIDHLEAALPL 486
RESULT 12
LAC3_TRAVI STANDARD; PRT; 473 AA.
ID LAC3_TRAVI
AC Q99049;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase 3 precursor (EC 1.10.3.2) (Benzenediol:oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCC3
OS Trametes villosa (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=47662;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97128774; PubMed=8973314;
RA Yaver D.S., Golightly E.J.;
RT "Cloning and characterization of three laccase genes from the
RT white-rot basidiomycete *Trametes villosa*: genomic organization of the
RT laccase gene family.";
RL Gene 181:95-102(1996).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC -----

```

QY 480 VPKAWSDLCPYID 492
   ||: ||: ||: ||:
Db 454 VPDWNLCPYTFD 466

RESULT 13
LAC2_AGABI
ID LAC2_AGABI STANDARD; PRP; 520 AA.
AC Q12542;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase II precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (brishniol oxidase) (Diphenol oxidase).
GN LCC2.
OS Eukaryota; Fungi; Basidiomycota; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_TaxID=5341,
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=D649;
RC MEDLINE=93367392; PubMed=8360614;
RA Perry C.R., Smith M., Britnell C.H., Wood D.A., Thurston C.F.;
RT "Identification of two laccase genes in the cultivated mushroom
RT Agaricus bisporus.";
RL J. Gen. Microbiol. 139:1209-1218(1993).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzenesemiquinone + 2
CC H(2)O.
CC -1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L10663; AAA17035.1; -
CC HSPSP; P37064; IASQ
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; Multicu_Oxidase2.
CC Pfam: PF00394; Cu-oxidase; 3.
CC PROSITE: PS00079; MULTICOPPER_OXIDASE1; 2.
CC PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
CC Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
CC Glycoprotein; Repeat; Multigene family.
CC SIGNAL 1
FT CHAIN 20 520 LACCASE II.
FT DOMAIN 21 145 PLASTOCYANIN-LIKE 1.
FT DOMAIN 157 305 PLASTOCYANIN-LIKE 2.
FT DOMAIN 375 488 PLASTOCYANIN-LIKE 3.
FT METAL 82 82 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 84 84 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 127 127 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129 129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 417 417 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 420 420 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 422 422 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 470 470 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 471 471 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 472 472 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 476 476 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 108 108 N-LINKED (GLNAC... ) (POTENTIAL).
FT CARBOHYD

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FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 520 AA; 57822 MW; EF100145F0A697AA CRC64;

Query Match 45.7%; Score 1219.5; DB 1; Length 520;
Best Local Similarity 49.0%; Pred. No. 7.8e-80;
Matches 251; Conservative 70; Mismatches 140; Indels 51; Gaps 15;

QY 10 VANAPVSPDGLRDAIVVGVPSPLITGKGRFQNLNVVDLTINHSMLKSTSIHHGFF 69
Db 28 LVNTRLPADGERTVTVINGEFTGLVQVNGKDSVRIPVANKLTSFTRRSVSIHHGFF 87
QY 70 QAGTNWADGPAFVNCQPIASGHSFLYDFHPVDAQAGTGFYHSHLSYQCDGLRGFFVYDP 129
Db 88 QARTSGDGPFAFVNCQPPNTTTFEVSVADESFTGFYHSHLSYQCDGLRGAFVYDP 147
QY 130 KDPHASRYVDNVESTVITLTDWYHTAA--RLGPRFPLG----ADATLINGLGRSASTPTA 183
Db 148 RDLRLHLYDVDDSTVITLAEWYHILAPDATNEFFSSGIIIPVDSGLNGKRGNGGLT 207
QY 184 ALAVINQHGKRYRFLVSVISCDPNYTFSDIGNLTIVIEDGINSOPLLVDSIQIFAAR 243
Db 208 PFVAVNVRGKRYRLVRIASISCRFFTFSDVNHSLVFEADGVHDPVQVNVDIYAAAR 267
QY 244 YSFVLNANQTVGNVWRA-----NPNFGTVGFAGGINSAILRYOGAPVAEPTTQT 294
Db 268 VSVILHANQPIDNWIRAPMTGGNDRPNLNI-----SLTALILRYHGAREVETTVN- 321
QY 295 TSVIP---LIETNLHPLARMPVPGSPTPGGVDK--ALMLAFNFGNFTFINNATPTPTV 349

RESULT 14
LACL_AGABI STANDARD; PRT; 520 AA.
AC Q12541;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Laccase I precursor (EC 1.10.3.2) (benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
GN LCC1.
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OX NCBI_TaxID=5341;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=D649; TISSUE=Mycelium;
RX MEDLINE=93367392; PubMed=8360614;
RA Perry C.R., Smith M., Britnell C.H., Wood D.A., Thurston C.F.;
RT Identification of two laccase genes in the cultivated mushroom
RT Agaricus bisporus.
RL J. Gen. Microbiol. 139:1209-1218(1993).
CC -I- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE).
CC -I- CATALYTIC ACTIVITY: 4 benzenediol + O(2) = 4 benzosemiquinone + 2
CC H(2)O.
```

```
CC -I- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -I- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; L10664; AAC18877.1; -.
DR HSP; P37064; IAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu_oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
KW Glycoprotein; Repeat; Multigene family.
FT SIGNAL 1..19
FT CHAIN 20..520 LACCASE I.
FT DOMAIN 21..145 PLASTOCYANIN-LIKE 1.
FT DOMAIN 157..305 PLASTOCYANIN-LIKE 2.
FT DOMAIN 375..488 PLASTOCYANIN-LIKE 3.
FT METAL 82..82 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 84..84 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 127..127 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 129..129 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 147..147 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 171..171 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 199..199 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 227..227 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 255..255 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 283..283 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 311..311 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 339..339 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 367..367 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT METAL 395..395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT METAL 423..423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT METAL 451..451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT METAL 479..479 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 520 AA; 58099 MW; 943DB3F23297B891 CRC64;

Query Match 44.7%; Score 1192.5; DB 1; Length 520;
Best Local Similarity 48.1%; Pred. No. 6.6e-78;
Matches 245; Conservative 71; Mismatches 148; Indels 45; Gaps 14;

QY 10 VANAPVSPDGLRDAIVVGVPSPLITGKGRFQNLNVVDLTINHSMLKSTSIHHGFF 69
Db 28 LVNTRLPADGERTVTVINGEFTGLVQVNGKDSVRIPVANKLTSFTRRSVSIHHGFF 87
QY 70 QAGTNWADGPAFVNCQPIASGHSFLYDFHPVDAQAGTGFYHSHLSYQCDGLRGFFVYDP 129
Db 88 QARTSGDGPFAFVNCQPPNTTTFEVSVADESFTGFYHSHLSYQCDGLRGAFVYDP 147
QY 130 KDPHASRYVDNVESTVITLTDWYHTAA--RLGPRFPLG----ADATLINGLGRSASTPTA 183
Db 148 RDLRLHLYDVDDSTVITLAEWYHILAPDATNEFFSSGIIIPVDSGLNGKRGNGGLT 207
QY 184 ALAVINQHGKRYRFLVSVISCDPNYTFSDIGNLTIVIEDGINSOPLLVDSIQIFAAR 243
Db 208 PFVAVNVRGKRYRLVRIASISCRFFTFSDVNHSLVFEADGVHDPVQVNVDIYAAAR 267
QY 244 YSFVLNANQTVGNVWRA-----NPNFGTVGFAGGINSAILRYOGAPVAEPTTQT 294
Db 268 VSVILHANQPIDNWIRAPMTGGNDRPNLNI-----SLTALILRYHGAREVETTVN- 321
QY 295 TSVIP---LIETNLHPLARMPVPGSPTPGGVDK--ALMLAFNFGNFTFINNATPTPTV 349
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Db 322 ---VPGKLLDQEMHPI-RQEGPKGLGDPDPKHITLNLIA-OPNAPFFDINGISYISPTV 376
QY 350 PVLQILISGTAQADLLPAGSVPLPAHSHTIETLPATLAPAGPHFHLHGHAFAVRS 409
Db 377 PVLQILISGAKRPEDVLPQSIQIFVFKNSLIEYNIP-----GEGA-HPFHLHGHNFDVLA 431
QY 410 AGSTYNYNDPIFRDVTSTGTPAAGDNVTIRFOTDNPFGWFLHCHIDFHLDAAGFAIVFAE 469
Db 432 SDDTFNFKNPPRDVY----PINGGNTTFRFFDNPFCANFLHCHIDHLEAGLAIIVFAE 487
QY 470 DVADVKAANP-----VPKAWSDLCPYDGL 494
Db 488 APED-NVSGPQSQITPDQWDLCLPEYNAI 515

RESULT 15
LAC4_THACU
ID LAC4_THACU STANDARD; PRT; 531 AA.
CC Q02081;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Laccase 4 precursor (EC 1.10.3.2) (Benzenediol: oxygen oxidoreductase)
DE (Urishiol oxidase) (Diphenol oxidase).
OS LCC4.
GN Thanatephorus cucumeris (Black scurf of potato) (Rhizoctonia solani).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Heterobasidiomycetidae; Ceratobasidiales; Ceratobasidiaceae;
OC mitosporic Ceratobasidiaceae; Rhizoctonia.
NCBI_TaxID=107832;
RX SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN=RS22;
RX MEDLINE=96171523; PubMed=8598061;
RA Wahleithner J.A., Xu F., Brown K.M., Brown S.H., Golightly E.J.,
RA Halkier T., Kauppinen S., Pedersen A., Schmeller P.;
RT "The identification and characterization of four laccases from the
RT plant pathogenic fungus Rhizoctonia solani."
RL Curr. Genet. 29:395-403(1996).
CC -1- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
CC PRODUCTS (PROBABLE). THIS ISOZYME SHOWS OPTIMAL ACTIVITY AT PH 7.
CC -1- CATALYTIC ACTIVITY: 4 benzenediol + O(2) -> 4 benzosemiquinone + 2
CC H(2)O.
CC -1- COPACITOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU
CC CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE
CC 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: IN MYCELIA, AT A HIGHER LEVEL THAN LCC1, LCC2
CC AND LCC3.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 254277; CAA91042.1;
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002335; MultiCu_oxidase2.
CC Pfam: PF00394; Cu-oxidase; 3.
CC PROSITE: PS00079; MULTICOPPER_OXIDASE1; FALSE NEG.
CC PROSITE: PS00080; MULTICOPPER_OXIDASE2; FALSE NEG.
CC Oxidoreductase; Signal; Copper; Metal-binding; Glycoprotein; Repeat;
KW Lignin degradation; Multigene family; Polymorphism.
FT SIGNAL 1 19
FT CHAIN 20 531
FT DOMAIN 23 146 LACCASE 4.
FT PLASTOCYANIN-LIKE 1.
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FT DOMAIN 158 315 PLASTOCYANIN-LIKE 2.
FT DOMAIN 384 507 PLASTOCYANIN-LIKE 3.
FT METAL 83 83 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 85 85 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 128 128 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 427 427 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 430 430 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 432 432 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 479 479 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 480 480 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 481 481 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 484 484 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL ? ? COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 42 42 P -> S.
FT VARIANT 119 119 H -> R.
FT VARIANT 246 246 R -> S.
FT VARIANT 256 256 P -> L.
FT VARIANT 261 261 P -> A.
SQ SEQUENCE 531 AA; 57545 MW; 737339803F75AB19 CRC64;

Query Match 40.4%; Score 1077; DB 1; Length 531;
Best Local Similarity 47.3%; Pred. No. 1.2e-69;
Matches 223; Conservative 56; Mismatches 152; Indels 40; Gaps 10;

QY 10 VANAPVSPDGLRDAIVVNGVPSPLITGKKGRFQNLVVDVTLTNHSLMKSSTSHHGFF 69
Db 29 IKVNVVAPDGFQRPVSVNGVLPGCTLTANKGDTLRVNTNQLTDPMSRRATTHHGLF 88
QY 70 QAGTNWADGPAFVNCQPIASGHFLYDFHVPDQAGTFWYHSHLSHTQVCDGLRGPFVYDP 129
Db 89 QATTADSDGPAFVTCQPIAQLNLTYSYIEPLHGTGTWYHAHLASQYVDGLRGPLVYDP 148
QY 130 KDPHASRYDVNDNESTVITLTDWYHT-----AARLGPFPGLDADFNLGLG 175
Db 149 NDPKHSRYDVDDASTVVMLEDVHTPAPVLEKQMFSTNTALLSP-----VPDSGLINGK 204
QY 176 RSASTPFAALAVINQHGKRYRFLVSIQDPNTVTFSDGHNLTVIEVDGINSOPLLVDS 235
Db 205 RYVGGPAPRPSVINVKRGKRYRLRVINASAIGSTFSEIGHRLTVIEADGTPHQLPVD 264
QY 236 IQIFAAQRYSEVLNANOTGVNVRANPNFGTVGFAGGINS-----ATLRQGPAPVPEPT 291
Db 265 FQIYAGQRYSVIVEANOTAANYWIRAPMTVAGAGTNANLDPTNVFVVLHTEGAPNAEPT 324
QY 292 TQTSV-IPLIETNLHPLARMPVPGSPPTGGVDKALNLFNFGTN----FFINNAFTP 346
Db 325 EQGSAIGTALVEENLHALINPGAPGGSAP--ADVSLNLAIGRSTVDGILRFTFNKVEA 382
QY 347 PTPVPLIQL-SGAOTQADLLPAGSVPLPAHSHTIETLPATLAPAGPHFHLHGHAFA 405
Db 383 PSLPTLKIILANNASNDADFTPNHHTIVLPHNKVI-----GAQHHRGADPHIHLGHVFD 437
QY 406 VRSAGSTTVNYNDPIFRDVTSTGTPAAGDNVTIRFOTDNPFGWFLHCHID 456
Db 438 IVKSLGGTTP-NYVNPFRDVRVG-----GTGVVLRFKADNPGPWFVCHID 483
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Search completed: December 14, 2002, 08:26:12
Job time : 31 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:19:36 ; Search time 263 Seconds
(without alignments)
12844.097 Million cell updates

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Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgggcggtggcgag.....tgagcagggtcaaccagtga 1500

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Database :
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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	%		Length	DB	ID	Description
		Query	Match				
1	1500	100.0	100.0	1500	21	AA09191	Trametes versicolo
2	1500	100.0	100.0	1500	24	ABA92910	Trametes versicolo
3	246	16.4	2880	17	AA715599		Laccase-LCC2 gene.
4	158	10.5	7986	20	AA223937		T. versicolor lacc
5	38	2.5	1563	24	ABL60268		Trametes versicolo
6	38	2.5	2418	17	AA715598		Laccase-LCC1 gene.
7	38	2.5	5762	20	AA223938		T. versicolor lacc
8	35	2.3	1497	11	AA003367		Phenol oxidase (PO
9	35	2.3	1497	11	AA003371		Sequence encoding

XX Claim 9; Page 17-19; 34pp; English.

PS The Trametes versicolor laccase gene can be used to create transgenic

CC plants which produce laccase at levels of about 0.01% or higher of the

CC total soluble protein of the plant. The transgenic plants may be used

CC for the large scale production of laccase enzymes. Laccase is mainly

CC used in the paper and pulp industry for breaking down lignin.

CC Conversely, laccase is also involved in lignin biosynthesis and the

CC formation of lignin polymers. It is therefore useful as a biological

CC adhesive for gluing wood (e.g. in the production of plywood, oriented

CC strand board, particle board and medium density fiberboard). Laccase

CC may also be used for catalyzing the oxidation of compounds such as

CC o,p-diphenols, aminophenols, polyamines and inorganic ions. It is

CC also used as a marker enzyme in enzyme immunoassays, for the oxidation

CC of steroids and the synthesis of vinblastine (a cytostatic compound

CC used in treating malignant diseases).

XX

SQ Sequence 1500 BP; 275 A; 551 C; 402 G; 272 T; 0 other;

Query Match 100.0%; Score 1500; DB 21; Length 1500;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCATCGGGCGGTGGCGAGCCTCGTCTCGGGAACGCCCGCTCGCCGAGGGTTC 60

DB 1 GCCATCGGGCGGTGGCGAGCCTCGTCTCGGGAACGCCCGCTCGCCGAGGGTTC 60

QY 61 CTTCCGGATGCCATCGTGGTCAACGGGTGGTCCCTTCGCCGCTCATCCGGGAAGAAG 120

DB 61 CTTCCGGATGCCATCGTGGTCAACGGGTGGTCCCTTCGCCGCTCATCCGGGAAGAAG 120

QY 121 GGAGACCGCTTCCAGCTCAACGCTCGTGGACACCTTGACCAACACAGCATGCTCAAGTCC 180

DB 121 GGAGACCGCTTCCAGCTCAACGCTCGTGGACACCTTGACCAACACAGCATGCTCAAGTCC 180

QY 181 ACTAGTATCACTGGCAGCGCTTCTCCAGGAGGACCAACTGGGCGAGACGCCGG 240

DB 181 ACTAGTATCACTGGCAGCGCTTCTCCAGGAGGACCAACTGGGCGAGACGCCGG 240

QY 241 TTGCTCAACAGTGCCTATTGCTTCGGGCACTTCTTCTGTACGACTTCCATGTGCC 300

DB 241 TTGCTCAACAGTGCCTATTGCTTCGGGCACTTCTTCTGTACGACTTCCATGTGCC 300

QY 301 GACGAGCAGGAAGTGTCTGGTACCAAGTATCTGTCTACGCAATACTGTGAGGGCTG 360

DB 301 GACGAGCAGGAAGTGTCTGGTACCAAGTATCTGTCTACGCAATACTGTGAGGGCTG 360

QY 361 CGAGGACCGTTCGCTGTAGGACCCCAAGATCCGACGCCGCCCTACGATGTTGAC 420

DB 361 CGAGGACCGTTCGCTGTAGGACCCCAAGATCCGACGCCGCCCTACGATGTTGAC 420

QY 421 AACGAGACGAGTTCATCAGCTTGACGACTGGTACCACACCGCTGCCGCTCGGTCC 480

DB 421 AACGAGACGAGTTCATCAGCTTGACGACTGGTACCACACCGCTGCCGCTCGGTCC 480

QY 481 AGGTTCCCACTGGCGGCGACGCTCATCAATGGTCTTGGGGGCTGGGCTCCACT 540

DB 481 AGGTTCCCACTGGCGGCGACGCTCATCAATGGTCTTGGGGGCTGGGCTCCACT 540

QY 541 CCCACCGCGGCTTGTGTATCAAGTCCAGCAGCAAGGCGCTACCGCTTCCGCTC 600

DB 541 CCCACCGCGGCTTGTGTATCAAGTCCAGCAGCAAGGCGCTACCGCTTCCGCTC 600

QY 601 GTTTCGATCTCGTCGACCGGACTACAGCTTCAGATCCGAGGCAATCTCAGCGTC 660

DB 601 GTTTCGATCTCGTCGACCGGACTACAGCTTCAGATCCGAGGCAATCTCAGCGTC 660

QY 661 ATCGAGGTGACGGTATCAACAGCCGCTCTCTTGTGCACTCTATCCAGATCTTCGCC 720

DB 661 ATCGAGGTGACGGTATCAACAGCCGCTCTCTTGTGCACTCTATCCAGATCTTCGCC 720

QY 721 GCGAGGCGCTACTCCTTTGTTGATGCGAACCAACGCTCGGCAACTACTGGGTCCG 780

DB 721 GCGAGCGCTACTCCTTTGTTGAATGCAACCAACGCTCGGCAACTACTGGGTCCG 780

QY 781 GCGAACCCGAACTTCGGAACGGTTGGTTCGCGGGGGATCAACTCCGCATCTCTCGC 840

DB 781 GCGAACCCGAACTTCGGAACGGTTGGTTCGCGGGGGATCAACTCCGCATCTCTCGC 840

QY 841 TACCAAGGCGACAGTTCGCGAGCCCACTACGACCCAGACGCTCGGTGATCCCGCTT 900

DB 841 TACCAAGGCGACAGTTCGCGAGCCCACTACGACCCAGACGCTCGGTGATCCCGCTT 900

QY 901 ATGAGACGAACTTCGACCCCTTCGCTCGCATGCTGCTGGCAGCCGACACCGGG 960

DB 901 ATGAGACGAACTTCGACCCCTTCGCTCGCATGCTGCTGGCAGCCGACACCGGG 960

QY 961 GCGTCTGACAAGGCGCTCAACCTCGCTTAACTTCAACGCGACCAACTTCTTCATCAAC 1020

DB 961 GCGTCTGACAAGGCGCTCAACCTCGCTTAACTTCAACGCGACCAACTTCTTCATCAAC 1020

QY 1021 AACGCGACTTTCAGCGCGCGACCGTCCCGTACTCTCCAGATTTCTGAGCGTGCAG 1080

DB 1021 AACGCGACTTTCAGCGCGCGACCGTCCCGTACTCTCCAGATTTCTGAGCGTGCAG 1080

QY 1081 ACCGCAACAGCTGCTCCCTGCAAGGCTCTGTACTACCGCTCCGCGCCACTCCACCATC 1140

DB 1081 ACCGCAACAGCTGCTCCCTGCAAGGCTCTGTACTACCGCTCCGCGCCACTCCACCATC 1140

QY 1141 GAGATCAGCTGCGCGCGACCGCTTGGCGCGGGTGCACGCGACCGCTTCCACCTGCAC 1200

DB 1141 GAGATCAGCTGCGCGCGACCGCTTGGCGCGGGTGCACGCGACCGCTTCCACCTGCAC 1200

QY 1201 GGTACGCGCTTCCGCGTTCGTCAGCGCGGGGAGCACCGTATAACTACAAGACCG 1260

DB 1201 GGTACGCGCTTCCGCGTTCGTCAGCGCGGGGAGCACCGTATAACTACAAGACCG 1260

QY 1261 ATCTTCGCGAGCTGTGAGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320

DB 1261 ATCTTCGCGAGCTGTGAGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320

QY 1321 TTCAGACGACAAACCCCGCGGTGTTCTTCCACTGCGCACATCGACTTCCACCTGCAC 1380

DB 1321 TTCAGACGACAAACCCCGCGGTGTTCTTCCACTGCGCACATCGACTTCCACCTGCAC 1380

QY 1381 CGCGGCTTCGCGATCGTGTTCGAGAGGAGCTTCCGAGCGTGAAGCGCGGAAACCGGTT 1440

DB 1381 CGCGGCTTCGCGATCGTGTTCGAGAGGAGCTTCCGAGCGTGAAGCGCGGAAACCGGTT 1440

QY 1441 CCGAAGCGGTGTCGAGCTGTCCCGATCTACGACGGGCTGACGAGGCTAACCACTGA 1500

DB 1441 CCGAAGCGGTGTCGAGCTGTCCCGATCTACGACGGGCTGACGAGGCTAACCACTGA 1500

RESULT 2

ABA92910

ID ABA92910 standard; cDNA; 1500 BP.

XX

XX ABA92910;

XX AC

XX AC

DT 09-APR-2002 (first entry)

XX

DE Trametes versicolor laccase I gene.

XX

KW Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;

KW copper; metal cofactor; gene; plant; ds.

XX

OS Trametes versicolor.

XX

Key Location/Qualifiers

FF 1..1500

FF CDS

FF /*tag= a

FF /partial

FF /product= "laccase I"

FF /note= "no start codon given"

[illegible]

```

RESULT 3
AAAT15599
ID AAAT15599 standard; DNA; 2880 BP.
XX
AC AAAT15599;
XX
DT 07-APR-1996 (first entry)
XX
DE Laccase-LCC2 gene.
XX
KW Laccase-LCC2; Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pBSY19;
KW lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ss.
XX
OS Polyporus pinsitus.
OS Trametes villosa.
XX
FH Key
FH CDS Location/Qualifiers
FT 364..2492
FT /*tag= a
FT /product= Laccase-LCC2
FT /note= "EC-1.10.3.2"
FT sig_peptide
FT 364..423
FT /*tag= b
FT 364..543
FT /*tag= c
FT 544..592
FT /*tag= d
FT 593..661
FT /*tag= e
FT 662..715
FT /*tag= f
FT 716..835
FT /*tag= g
FT 836..899
FT /*tag= h
FT 900..1013
FT /*tag= i
FT 1014..1066
FT /*tag= j
FT 1067..1132
FT /*tag= k
FT 1133..1187
FT /*tag= l
FT 1188..1283
FT /*tag= m
FT 1284..1343
FT /*tag= n
FT 1344..1498
FT /*tag= o
FT 1499..1553
FT /*tag= p
FT 1554..1751
FT /*tag= q
FT 1752..1815
FT /*tag= r
FT 1816..1872
FT /*tag= s
FT 1873..1928
FT /*tag= t
FT 1929..2135
FT /*tag= u
FT 2136..2195
FT /*tag= v
FT 2196..2492
FT /*tag= w
XX
PN WO9600290-A1.
XX

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PD 04-JAN-1996.
XX
PF 15-JUN-1995; 95WO-US07536.
XX
PR 15-MAY-1995; 95US-0441147.
PR 24-JUN-1994; 94US-0265534.
XX
PA (NOVO ) NOVO NORDISK BIOTECH INC.
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
XX
WPI; 1996-068874/07.
P-PSDB; AAR90722.
XX
DNA constructs for expression of Polyporus laccase enzymes - for use
in e.g. lignin manipulation, juice mir., phenol polymerisation and
phenol resin prodn
XX
PS Claim 5; Page 62-65; 137pp; English.
XX
CC The sequence encodes laccase-LCC2 (pi 5.95) from Polyporus pinsitus
CC (Trametes villosa). Polymerase chain reaction (PCR) amplification of
CC P. pinsitus cDNA using primers 3331 (AAAT15603) and 3332 (AAAT15604) gives
CC a 1500 bp fragment, which is joined to a signal peptide sequence
CC from a 43-kDa cellulase using primer PHD433 (AAAT15605) and a pUC
CC forward primer in PCR. Clones are expressed in Aspergillus oryzae,
CC and a cDNA probe is obtained and used to screen a P. pinsitus
CC genomic library in Escherichia coli DH5-alpha, giving plasmid
CC pDSY19 (23GEN), with a 4-kb HindIII insert (NRRL B-21266).
CC Screening also results in isolation of LCC1 (AAAT15598) and LCC3-LCC5
CC (AAAT15600-T15602), which encode different laccases produced by P.
CC pinsitus. The laccases may be used to polymerise lignin or
CC lignosulphonates, to depolymerise Kraft pulp, to oxidise dyes or
CC precursors, in hair dye compositions, or to polymerise or oxidise a
CC phenolic or aniline compound. These new laccases are well-expressed
CC in Aspergillus spp. (with vector integration in the genome), in
CC contrast to previous basidiomycete laccases, which give low yields
CC of recombinant enzyme.
XX
SQ Sequence 2880 BP; 547 A; 908 C; 793 G; 632 T; 0 other;
Query Match 16.4%; Score 246; DB 17; Length 2880;
Best Local Similarity 99.7%; Pred. No. 6.4e-109;
Matches 296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1204 CACGCCCTTCGGCGTCTTCGACGGGGGAGCACCACGTATACACACCGGATC 1263
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1264 TTCGCGGACGTCGTGAGCACGGGCACGCCCGCGGGGACACGTACGCGCTTC 1323
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1265 TTCGCGGACGTCGTGAGCACGGGCACGCCCGCGGGGACACGTACGCGCTTC 2315
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1324 CAGACGGACACCCCGGGCGCGTGTCTCCACTGCCACATCGACTTCACCTCGACGG 1383
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1384 GGCTTCGGGATCGTTCGACAGGACGTTGCGGACGTGAAGCGGCGAACCCGGTTCG 1443
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1444 RAGGCGTGTGCGACCTGTGCCCGGATCTACGACGGGCTCAGCGAGGCTAACAGTGA 1500
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1445 RAGGCGTGTGCGACCTGTGCCCGGATCTACGACGGGCTCAGCGAGGCTAACAGTGA 2492
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
RESULT 4
AAZ23937
ID AAZ23937 standard; DNA; 7986 BP.
XX
AC AAZ23937;
XX

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```
DT 27-JAN-2000 (first entry)
XX T. versicolor laccase I DNA.
DE Filamentous fungus; hydrolytic enzyme; cellulase; hemicellulase;
KW lipase; oxidoreductase; lignin peroxidase; mangan peroxidase;
KW cellobiose-chinon oxidoreductase; cellobiose-oxidase; laccase I; ss.
XX Trametes versicolor.
OS W09951757-A1.
XX
PN 14-OCT-1999.
XX
PD 01-APR-1999; 99WO-EP02252.
XX
PF 02-APR-1998; 98DE-1014853.
XX
PR (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
XX Pfaller R, Hessing J, Van Den Hondel C, Van Gorcom R;
PI WPI; 1999-633742/54.
XX
XX An expression system for the production of proteins in filamentous
PT fungi -
XX
PS Claim 8; Page 50-53; 67pp; German.
XX
XX This invention describes a novel expression system for the production
CC of a protein in a filamentous fungus which comprises a Trametes or
CC Polyporus host organism, a DNA vector containing a positive selection
CC marker and a DNA vector containing a gene of interest controlled by an
CC active genetic regulation element in the host organism. The fungi are
CC useful for the production of hydrolytic enzymes, e.g. cellulases,
CC hemicellulase and lipases or oxidoreductases, e.g. lignin peroxidase,
CC mangan peroxidase, laccase, cellobiose-chinon oxidoreductase or
CC cellobiose-oxidase. This sequence represents the laccase I nucleic acid
CC sequence isolated from Trametes versicolor.
XX
SQ Sequence 7986 BP; 1698 A; 2404 C; 2107 G; 1777 T; 0 other;

Query Match 10.5%; Score 158; DB 20; Length 7986;
Best Local Similarity 100.0%; Pred. No. 2.3e-66;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 GCTACCGCTTCGCTCGTTTCGATCTCGTGGACCCGAACTACAGTTTCAGCATCGAGC 643
DB 2170 GCTACCGCTTCGCTCGTTTCGATCTCGTGGACCCGAACTACAGTTTCAGCATCGAGC 2229

QY 644 GGCACAATCTGACCGTCATCGAGGTGCGAGGTATCAACAGCCAGCCTCTCTTGTGCGACT 703
DB 2230 GGCACAATCTGACCGTCATCGAGGTGCGAGGTATCAACAGCCAGCCTCTCTTGTGCGACT 2289

QY 704 CTATCCAGATCTTGGCGCGCGAGCGCTACTCTCTTGTG 741
DB 2290 CTATCCAGATCTTGGCGCGCGAGCGCTACTCTTGTG 2327

RESULT 5
ABL60268
ID ABL60268 standard; cDNA; 1563 BP.
XX
XX ABL60268;
AC
XX
XX 23-AUG-2002 (first entry)
XX Trametes versicolor Laccase III encoding cDNA SEQ ID NO 25.
DE
XX Fungi; Thal; Ctal; copper-dependent secreted protein; copper; laccase;
KW Trametes ATR1 homologue; copper transporting ATPase; gene; ss.
XX
XX Trametes versicolor.
OS
```

```
XX Key Location/Qualifiers
FH 1..1563
FT /*tag= a
FT /product= "Laccase Iii"
XX
PN DE10046932-A1.
XX
XX 16-MAY-2002.
XX
XX 21-SEP-2000; 2000DE-1046932.
XX
XX 21-SEP-2000; 2000DE-1046932.
XX
XX (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
XX Marbach-Ringhandt K, Pfaller R, Uldschmid A;
PI WPI; 2002-445163/48.
XX
XX P-PSDB; ABE77510.
DR
XX Expression system for increased production of copper-dependent enzymes,
PT particularly laccase, includes the gene for a copper homeostasis
PT protein -
XX
XX Example 9; Page 46-48; 58pp; German.
XX
XX The invention relates to an expression system (A) that provides increased
CC expression of copper-dependent secreted proteins (I) in eukaryotic cells
CC comprises a gene (II) that encodes (I) and at least one cooper
CC homeostasis gene (III). (A) is used to express enzymes, especially
CC laccase, that require copper as co-factor. (III) transports copper to the
CC secretory pathway so its overexpression leads to increased yields of (I).
CC The present sequence is that of the Trametes versicolor Laccase III
CC encoding polynucleotide of the invention.
XX
SQ Sequence 1563 BP; 271 A; 603 C; 384 G; 305 T; 0 other;

Query Match 2.5%; Score 38; DB 24; Length 1563;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCTCCACATGCCACATCGACTTCCACCTCGA 1379
DB 1405 CCGTGGTTCTCCACATGCCACATCGACTTCCACCTCGA 1442

RESULT 6
AAT15598
ID AAT15598 standard; DNA; 2418 BP.
XX
XX AAT15598;
AC
XX 07-APR-1996 (first entry)
DT
XX Laccase-LCC1 gene.
DE
XX
XX Laccase-LCC1: Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pDSY18;
KW lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ds.
XX
XX Polyporus pinsitus.
OS
XX Trametes villosa.
XX
XX Key Location/Qualifiers
FH CAAT_signal 19..22
FT /*tag= a
FT TATA_signal 129..134
FT /*tag= b
FT CDS 231..2223
```

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FT FT /*tag= c
FT FT /product= Laccase-LCC1
FT FT /note= "EC-1.10.3.2"
FT FT 231..293
FT FT /*tag= d
FT FT 231..413
FT FT /*tag= e
FT FT 414..464
FT FT /*tag= f
FT FT 465..533
FT FT /*tag= g
FT FT 534..589
FT FT /*tag= h
FT FT 590..709
FT FT /*tag= i
FT FT 710..764
FT FT /*tag= j
FT FT 765..878
FT FT /*tag= k
FT FT 879..934
FT FT /*tag= l
FT FT 935..1000
FT FT /*tag= m
FT FT 1001..1050
FT FT /*tag= n
FT FT 1051..1146
FT FT /*tag= o
FT FT 1147..1197
FT FT /*tag= p
FT FT 1198..1353
FT FT /*tag= q
FT FT 1354..1410
FT FT /*tag= r
FT FT 1411..1610
FT FT /*tag= s
FT FT 1609..1662
FT FT /*tag= t
FT FT 1663..2223
FT FT /*tag= u
XX XX W09600290-A1.
XX XX 04-JAN-1996.
XX XX 15-JUN-1995; 95WO-US07536.
XX XX 15-MAY-1995; 95US-0441147.
XX XX 24-JUN-1994; 94US-0265534.
XX XX (NOVO ) NOVO NORDISK BIOTECH INC.
XX XX (NOVO ) NOVO-NORDISK AS.
XX XX Aaslyng DA, Dalbøge H, Schneider P, Xu F, Yaver DS;
XX WPI; 1996-068874/07.
XX P-PSDB; AAR90721.
XX DNA constructs for expression of Polyporus laccase enzymes - for use
XX in e.g. lignin manipulation, juice mfr., phenol polymerisation and
XX phenol resin prodn
XX Claim 3; Page 57-60; 137pp; English.
XX The sequence encodes laccase-LCC1 (pI 4.49) from Polyporus pinsitus
XX (Trametes villosa). Polymerase chain reaction (PCR) amplification of
XX P. pinsitus cDNA using primers 3331 (AAT15603) and 3332 (AAT15604) gives
XX a 1500 bp fragment, which is joined to a signal peptide sequence
XX from a 43-kDa cellulase using primer pHD433 (AAT15605) and a pUC
XX forward primer in PCR. Clones are expressed in Aspergillus oryzae,
XX and a cDNA probe is obtained and used to screen a P. pinsitus
XX genomic library in Escherichia coli XL1-Blue, giving plasmid pDSY18
XX (21GEN) with an 8.0-kb BamHI insert (NRRL B-21265). Screening also
XX results in isolation of LCC2-LCC5 (AAT15599-T15602), which encode
```

```
CC different laccases produced by P. pinsutus. The laccases may be
CC used to polymerise lignin or lignosulphonates, to depolymerise
CC kraft pulp, to oxidise dyes or precursors, in hair dye
CC compositions, or to polymerise or oxidise a phenolic or aniline
CC compound. These new laccases are well-expressed in Aspergillus
CC spp. (with vector integration in the genome), in contrast to
CC previous basidiomycete laccases, which give low yields of
CC recombinant enzyme.
XX XX Sequence 2418 BP; 465 A; 799 C; 589 G; 565 T; 0 other;
SQ Query Match 2.5%; Score 38; DB 17; Length 2418;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
DB 2065 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 2102
RESULT 7
AAZ23938
ID AAZ23938 standard; DNA; 5762 BP.
XX AC AAZ23938;
XX 27-JAN-2000 (first entry)
XX T. versicolor laccase III DNA.
XX Filamentous fungus; hydrolytic enzyme; cellulase; hemicellulase;
XX lipase; oxidoreductase; lignin peroxidase; mangan peroxidase;
XX cellobiose-chinon oxidoreductase; cellobiose-oxidase; laccase III; ss.
XX Trametes versicolor.
XX WO9951757-A1.
XX 14-OCT-1999.
XX 01-APR-1999; 99WO-EP02252.
XX 02-APR-1998; 98DE-1014853.
XX (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
XX Pfaller R, Hessing J, Van Den Hondel C, Van Gorcom R;
XX WPI; 1999-633742/54.
XX An expression system for the production of proteins in filamentous
XX fungi -
XX Claim 8; Page 53-55; 67pp; German.
XX This invention describes a novel expression system for the production
XX of a protein in a filamentous fungus which comprises a Trametes or
XX Polyporus host organism, a DNA vector containing a positive selection
XX marker and a DNA vector containing a gene of interest controlled by an
XX active genetic regulation element in the host organism. The fungi are
XX useful for the production of hydrolytic enzymes, e.g. cellulases,
XX hemicellulase and lipases or oxidoreductases, e.g. lignin peroxidase,
XX mangan peroxidase, laccase, cellobiose-chinon oxidoreductase or
XX cellobiose-oxidase. This sequence represents the laccase III nucleic acid
XX sequence isolated from Trametes versicolor.
XX Sequence 5762 BP; 1113 A; 1781 C; 1644 G; 1224 T; 0 other;
SQ Query Match 2.5%; Score 38; DB 20; Length 5762;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
```


Db 2387 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 2424
|||||

RESULT 8
AAQ03367
ID AAQ03367 standard; DNA; 1497 BP.
XX
AC AAQ03367;
XX
DT 18-AUG-1990 (first entry)
XX
DE Phenol oxidase (PO) gene.
XX
KW Phenol oxidase (PO) gene; enzyme.
XX
PN JP02005877-A.
XX
PD 10-JAN-1990.
XX
PF 16-JUN-1988; 88JP-0149103.
XX
PR 16-JUN-1988; 88JP-0149103.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1950-053914/08.
XX
DR P-PSDB; AAR05279.
XX
PT Phenol oxidase gene - used for biological pulping, etc.
XX
PS Page 812-813; Fig 2; 14pp; Japanese.
XX

CC It can be used to transform various organisms to produce new organisms
CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridising to it, and recombinant DNA
CC consisting of this gene or AAN93367 ligated with vector DNA.
XX
SQ Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||

Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 9
AAQ03571
ID AAQ03571 standard; DNA; 1497 BP.
XX
AC AAQ03571;
XX
DT 03-FEB-1991 (first entry)
XX
DE Sequence encoding phenol oxidase (PO).
XX
KW Paper pulping; ds.
XX
PN JP02027986-A.
XX
PD 30-JAN-1990.
XX
PF 15-JUL-1988; 88JP-0175236.
XX
PR 15-JUL-1988; 88JP-0175236.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1950-323326/43.
XX

CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridising to it, and recombinant DNA
CC consisting of this gene or AAN93367 ligated with vector DNA.
XX
SQ Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||

Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 10
AAQ03572
ID AAQ03572 standard; DNA; 1497 BP.
XX
AC AAQ03572;
XX
DT 03-FEB-1991 (first entry)
XX
DE Sequence encoding phenol oxidase (PO).
XX
KW Paper pulping; ds.
XX
PN JP02027986-A.
XX
PD 30-JAN-1990.
XX
PF 15-JUL-1988; 88JP-0175236.
XX
PR 15-JUL-1988; 88JP-0175236.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1990-323326/43.
XX
DR P-PSDB; AAR07069.
XX
PT New phenol oxidase gene - has DNA encoding specified sequence of
XX 499 aminoacid(s)
XX
PS Claim 5; Fig 3; 15pp; Japanese.
XX
CC PO is useful in biological paper pulping and bleaching.
XX
SQ Sequence 1497 BP; 272 A; 536 C; 377 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||

Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 11
AAQ03366
ID AAQ03366 standard; DNA; 2049 BP.
XX
AC AAQ03366;
XX
DT 18-AUG-1990 (first entry)
XX
DE Phenol oxidase (PO) gene with introns.
XX
DR WPI; 1950-323326/43.
XX

CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridising to it, and recombinant DNA
CC consisting of this gene or AAN93367 ligated with vector DNA.
XX
SQ Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||

Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

DR P-PSDB; AAR07068.
XX
PT New phenol oxidase gene - has DNA encoding specified sequence of
XX 499 aminoacid(s)
XX
PS Claim 4; Fig 2; 15pp; Japanese.
XX
CC PO is useful in biological paper pulping and bleaching.
XX
SQ Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||

Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 10
AAQ03572
ID AAQ03572 standard; DNA; 1497 BP.
XX
AC AAQ03572;
XX
DT 03-FEB-1991 (first entry)
XX
DE Sequence encoding phenol oxidase (PO).
XX
KW Paper pulping; ds.
XX
PN JP02027986-A.
XX
PD 30-JAN-1990.
XX
PF 15-JUL-1988; 88JP-0175236.
XX
PR 15-JUL-1988; 88JP-0175236.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1990-323326/43.
XX
DR P-PSDB; AAR07069.
XX
PT New phenol oxidase gene - has DNA encoding specified sequence of
XX 499 aminoacid(s)
XX
PS Claim 5; Fig 3; 15pp; Japanese.
XX
CC PO is useful in biological paper pulping and bleaching.
XX
SQ Sequence 1497 BP; 272 A; 536 C; 377 G; 312 T; 0 other;

Query Match 2.3%; Score 35; DB 11; Length 1497;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||

Db 1342 CCCTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376

RESULT 11
AAQ03366
ID AAQ03366 standard; DNA; 2049 BP.
XX
AC AAQ03366;
XX
DT 18-AUG-1990 (first entry)
XX
DE Phenol oxidase (PO) gene with introns.
XX
DR WPI; 1950-323326/43.
XX

Phenol oxidase (PO) gene; enzyme.

XX Key Location/Qualifiers
FH exon 1..120
FT /*tag= a
FT /note="exon 1"
FT 121..176
FT /*tag= b
FT /note="intron 1"
FT 177..245
FT /*tag= c
FT /note="exon 2"
FT 246..297
FT /*tag= d
FT /note="intron 2"
FT 298..418
FT /*tag= e
FT /note="exon 3"
FT 419..480
FT /*tag= f
FT /note="intron 3"
FT 481..594
FT /*tag= g
FT /note="exon 4"
FT 595..648
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FT 649..712
FT /*tag= i
FT /note="exon 5"
FT 713..772
FT /*tag= j
FT /note="intron 5"
FT 773..868
FT /*tag= k
FT /note="exon 6"
FT 869..923
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FT /note="intron 6"
FT 924..1080
FT /*tag= m
FT /note="exon 7"
FT 1081..1136
FT /*tag= n
FT /note="intron 7"
FT 1137..1334
FT /*tag= o
FT /note="exon 8"
FT 1335..1390
FT /*tag= p
FT /note="intron 8"
FT 1391..1447
FT /*tag= q
FT /note="exon 9"
FT 1447..1497
FT /*tag= r
FT /note="intron 9"
FT 1498..1704
FT /*tag= s
FT /note="exon 10"
FT 1705..1755
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FT /note="intron 10"
FT 1756..2049
FT /*tag= u
FT /note="exon 11"
XX JF02005876-A.
PN
XX
XX 10-JAN-1990.
XX
XX 16-JUN-1988; 88JP-0149102.
PF
XX

PR 16-JUN-1988; 88JP-0149102.
XX
PA (OJIP) OJI PAPER KK.
XX
DR WPI; 1990-053913/08.
DR P-PSDB; AAR05279.
XX
PT Phenol oxidase gene - used for biological pulping, etc.
XX
PS Page 799-800; Fig 2; 12pp; Japanese.
XX
XX
CC It can be used to transform various organisms to produce new organisms
CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridising to it, and recombinant DNA
CC consisting of this gene or AAN93366 ligated with vector DNA.
XX
SQ Sequence 2049 BP; 386 A; 681 C; 499 G; 483 T; 0 other;
Query Match 2.3%; Score 35; DB 11; Length 2049;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCT 1376
|||||
Db 1894 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCT 1928
RESULT 12
AAQ03573
ID AAQ03573 standard; DNA; 2049 BP.
XX
AC AAQ03573;
XX
DT 15-AUG-1990 (first entry)
XX
DE Phenol oxidase gene.
XX
KW Phenol oxidase; biological pulping; bleaching; paper; ss.
XX
FH Key Location/Qualifiers
FT exon 1..121
FT /*tag= a
FT exon 177..245
FT /*tag= b
FT exon 298..418
FT /*tag= c
FT exon 481..594
FT /*tag= d
FT exon 649..712
FT /*tag= e
FT exon 773..868
FT /*tag= f
FT exon 924..1080
FT /*tag= g
FT exon 1137..1334
FT /*tag= h
FT exon 1391..1447
FT /*tag= i
FT exon 1498..1704
FT /*tag= j
FT exon 1756..2049
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FT exon 773..868
FT /*tag= l
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PN
XX
XX 30-JAN-1990.
XX
XX 15-JUL-1988; 88JP-0175235.
PF
XX
XX 15-JUL-1988; 88JP-0175235.
PR

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XX (OJIP ) OJI PAPER KK.
XX WPI; 1990-072975/10.
DR P-PSDB; AAR05668.
XX
XX DNA code for phenol oxidase gene - of specified
PT amino acid sequence is separated by introns.
XX
XX Claim 4; Page 2; 13pp; Japanese.
XX
XX Phenol oxidase encoded by the gene is used in biological
CC pulping and bleaching of paper.
XX
XX Sequence 2049 BP; 386 A; 681 C; 499 G; 483 T; 0 other;
SQ
Query Match 2.3%; Score 35; DB 11; Length 2049;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTCTCCACTGCCACATCGACTTCCACCT 1376
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 1894 CCGTGGTCTCCACTGCCACATCGACTTCCACCT 1928
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 13
AAT15602
ID AAT15602 standard; DNA; 2925 BP.
XX
AC AAT15602;
XX
DT 07-APR-1996 (first entry)
XX
DE Laccase-LCC5 gene.
XX
XX Laccase-LCC5; Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pDSY22;
KW plasmid pDSY23; lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ds.
XX
XX Polyporus pinsitus.
OS Trametes villosa.
OS
XX
XX Key Location/Qualifiers
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FT TATA_signal 438..442
FT /*tag= b
FT CDS 545..2810
FT /*tag= c
FT /*product= Laccase-LCC5
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FT sig_peptide 545..613
FT /*tag= d
FT exon 545..733
FT /*tag= e
FT intron 734..808
FT /*tag= f
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FT intron 878..932
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FT exon 1559..1714
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XX WO9600290-A1.
XX
XX 04-JAN-1996.
XX
XX 15-JUN-1995; 95WO-US07536.
XX
XX 15-MAY-1995; 95US-0441147.
PR 24-JUN-1994; 94US-0265534.
XX
XX (NOVO ) NOVO NORDISK BIOTECH INC.
PA (NOVO ) NOVO NORDISK AS.
XX
XX Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
XX
XX WPI; 1996-068874/07.
DR P-PSDB; AAR90725.
XX
XX DNA constructs for expression of Polyporus laccase enzymes - for use
in e.g. lignin manipulation, juice mfr., phenol polymerisation and
phenol resin prodn
XX
XX Claim 11; Page 78-81; 137pp; English.
XX
XX The sequence encodes laccase-LCC5 (pI 4.07) from Polyporus pinsitus
(CC Trametes villosa). Polymerase chain reaction (PCR) amplification of
(CC P. pinsutus cDNA using primers 3331 (AAT15603) and 3332 (AAT15604) gives
(CC a 1500 bp fragment, which is joined to a signal peptide sequence
(CC from a 43-kDa cellulase using primer PHD433 (AAT15605) and a pUC
(CC forward primer in PCR. Clones are expressed in Aspergillus oryzae,
(CC and a cDNA probe is obtained and used to screen a P. pinsutus
(CC genomic library in Escherichia coli DH5-alpha, giving plasmid
(CC pDSY22 (41GEN), with a 3.0-kb EcoRI insert (NRRL B-21263) and
(CC plasmid pDSY23 (41GEN), with a 4.5-kb MluI insert containing part of
(CC the pDSY22 insert and 5'-sequences. Screening also results in
(CC isolation of LCC1-LCC4 (AAT15598-T15601) which encode different
(CC laccases produced by P. pinsutus. The laccases may be used to
(CC polymerise lignin or lignosulphonates, to depolymerise Kraft pulp,
(CC to oxidise dyes or precursors, in hair dye compositions, or to
(CC polymerise or oxidise a phenolic or aniline compound. These new
(CC laccases are well-expressed in Aspergillus spp. (with vector
(CC integration in the genome), in contrast to previous basidiomycete
(CC laccases, which give low yields of recombinant enzyme.
XX

```

SQ Sequence 2925 BP; 554 A; 971 C; 734 G; 664 T; 2 other;

Query Match 2.3%; Score 35; DB 17; Length 2925;
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACT 1376
|||||
Db 2587 CCGTGGTTCCTCCACTGCCACATCGACTTCCACT 2621

RESULT 14

AA02671
ID AAX02671 standard; cDNA to mRNA; 1572 BP.

XX AC AAX02671;

DT 10-MAY-1999 (first entry)

DE T. versicolor laccase TV-1 cDNA from clone plac55.

XX Laccase; TV-1; delignification; pulp; depolymerisation; waste water;
KW high-molecular-weight aggregates; delinking; waste paper; polymerisation;
KW aromatic compound; lignin; pulp bleaching; oxidising dye; activating dye;
KW pigment formation; organic synthesis; ss.
XX

OS Trametes versicolour.

XX DE19724039-Al.

PD 10-DEC-1998.

XX 06-JUN-1997; 97DE-1024039.

XX 06-JUN-1997; 97DE-1024039.

PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.

XX Pfaller R, Wich G;

DR WPI; 1999-036087/04.

XX New DNA encoding Trametes versicolor laccase protein - used to e.g.
PT delignify pulp, depolymerise high molecular weight aggregates, delink
PT waste paper, polymerise aromatic compounds in waste water, activate
PT dyes and to couple organic compounds

XX Claim 1; Page 13-15; 42pp; German.

XX This invention describes novel laccase proteins isolated from Trametes
CC versicolor which can be used in methods for delignifying pulp,
CC depolymerising high-molecular-weight aggregates, delinking waste paper,
CC polymerising aromatic compounds in waste water (especially
CC lignin-containing waste water from pulp bleaching), oxidising dyes or
CC activating dyes for pigment formation, or in organic synthesis for
CC coupling aromatic compounds or for oxidising aromatic side chains.

XX Sequence 1572 BP; 270 A; 555 C; 427 G; 320 T; 0 other;

Query Match 2.2%; Score 33; DB 20; Length 1572;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCAC 1374

Db 1417 CCGTGGTTCCTCCACTGCCACATCGACTTCCAC 1449

RESULT 15

AA02672

ID AAX02672 standard; cDNA to mRNA; 1572 BP.

XX AC AAX02672;

XX

DT 10-MAY-1999 (first entry)

DE T. versicolor laccase TV-1 cDNA from clone plac56.

XX Laccase; TV-1; delignification; pulp; depolymerisation; waste water;
KW high-molecular-weight aggregates; delinking; waste paper; polymerisation;
KW aromatic compound; lignin; pulp bleaching; oxidising dye; activating dye;
KW pigment formation; organic synthesis; ss.
XX

OS Trametes versicolour.

XX DE19724039-Al.

PD 10-DEC-1998.

XX 06-JUN-1997; 97DE-1024039.

XX 06-JUN-1997; 97DE-1024039.

PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.

XX Pfaller R, Wich G;

DR WPI; 1999-036087/04.

XX New DNA encoding Trametes versicolor laccase protein - used to e.g.
PT delignify pulp, depolymerise high molecular weight aggregates, delink
PT waste paper, polymerise aromatic compounds in waste water, activate
PT dyes and to couple organic compounds

XX Claim 1; Page 15-17; 42pp; German.

XX This invention describes novel laccase proteins isolated from Trametes
CC versicolor which can be used in methods for delignifying pulp,
CC depolymerising high-molecular-weight aggregates, delinking waste paper,
CC polymerising aromatic compounds in waste water (especially
CC lignin-containing waste water from pulp bleaching), oxidising dyes or
CC activating dyes for pigment formation, or in organic synthesis for
CC coupling aromatic compounds or for oxidising aromatic side chains.

XX Sequence 1572 BP; 269 A; 558 C; 429 G; 316 T; 0 other;

Query Match 2.2%; Score 33; DB 20; Length 1572;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCAC 1374

Db 1417 CCGTGGTTCCTCCACTGCCACATCGACTTCCAC 1449

Search completed: December 14, 2002, 06:54:17

Job time : 294 secs

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 06:48:01 : Search time 2136 Seconds
(without alignments)
11373.235 Million cell updates/sec

Title: US-09-786-960-1

Perfect score: 1500

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	23	1.5	794	CNS03GCZ	AL242828 Tetraodon
c 2	22	1.5	523	AY105245	AY105245 Zea mays
c 3	22	1.5	530	BH774999	BH774999 fzmbo11fo
c 4	22	1.5	583	AW231821	AW231821 687042B12
c 5	21	1.4	264	AW102246	AW102246 EST211535
c 6	21	1.4	322	AY102246	AY102246 EST227946

c 7	21	1.4	341	9	AI412412	AI412412 EST240711
c 8	21	1.4	371	9	AA899112	AA899112 UI-R-E0-C
c 9	21	1.4	374	9	AI409646	AI409646 EST237938
c 10	21	1.4	381	9	AI234086	AI234086 EST230774
c 11	21	1.4	392	9	AI179240	AI179240 EST222931
c 12	21	1.4	397	9	AI103006	AI103006 EST212295
c 13	21	1.4	399	10	AW141507	AW141507 EST291561
c 14	21	1.4	401	10	BE110478	BE110478 UI-R-BJL-
c 15	21	1.4	401	12	BG371835	BG371835 UI-R-CV0-
c 16	21	1.4	401	13	BM389935	BM389935 UI-R-CN1-
c 17	21	1.4	402	12	BF544071	BF544071 UI-R-E0-C
c 18	21	1.4	404	9	AA944766	AA944766 EST200265
c 19	21	1.4	410	9	AI179051	AI179051 EST222734
c 20	21	1.4	418	9	AI179789	AI179789 EST223518
c 21	21	1.4	423	9	AI1010901	AI1010901 EST205352
c 22	21	1.4	429	9	AI1011109	AI1011109 EST210398
c 23	21	1.4	431	12	BG669875	BG669875 DRNALE07
c 24	21	1.4	435	9	AA851745	AA851745 EST194513
c 25	21	1.4	436	9	AI229927	AI229927 EST226622
c 26	21	1.4	440	9	AI008888	AI008888 EST203339
c 27	21	1.4	443	9	AI169426	AI169426 EST215277
c 28	21	1.4	446	12	BG670125	BG670125 DRNAQA11
c 29	21	1.4	449	9	AI229900	AI229900 EST226595
c 30	21	1.4	451	9	AI233932	AI233932 EST230620
c 31	21	1.4	452	9	AI407646	AI407646 EST235936
c 32	21	1.4	453	9	AI229540	AI229540 EST226235
c 33	21	1.4	455	9	AI231104	AI231104 EST227792
c 34	21	1.4	456	9	AI102729	AI102729 EST212018
c 35	21	1.4	457	9	AI145993	AI145993 UI-R-BT0-
c 36	21	1.4	462	9	AA859998	AA859998 UI-R-E0-C
c 37	21	1.4	462	9	AA900005	AA900005 UI-R-E0-C
c 38	21	1.4	463	9	AI180279	AI180279 EST224022
c 39	21	1.4	469	9	AI177784	AI177784 EST221437
c 40	21	1.4	471	9	AA944292	AA944292 EST199791
c 41	21	1.4	471	9	AI103271	AI103271 EST212560
c 42	21	1.4	471	9	AI230644	AI230644 EST227339
c 43	21	1.4	471	9	AI406329	AI406329 EST234615
c 44	21	1.4	490	9	AI177851	AI177851 EST221499
c 45	21	1.4	492	9	AI013026	AI013026 EST207477

ALIGNMENTS

RESULT 1	CNS03GCZ	794 bp	DNA	linear	GSS 17-MAY-2000
LOCUS	Tetraodon nigroviridis	genome survey sequence	PUC-ori	end of clone	024C10 of library G from Tetraodon nigroviridis, genomic survey
DEFINITION	sequence.				
ACCESSION	AL242828				
VERSION	AL242828.1	GI:7963597			
KEYWORDS	GSS; genome survey sequence.				
SOURCE	Tetraodon nigroviridis.				
ORGANISM	Tetraodon nigroviridis.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.				
AUTHORS	1 (bases 1 to 794)				
TITLE	Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.				
JOURNAL	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 794)				
TITLE	Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.				
JOURNAL	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis				
REFERENCE	Unpublished				

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REFERENCE 3 (bases 1 to 794)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
          scale clone-end sequencing project of the Tetraodon nigroviridis
          genome. For more information, please take a look at
          http://www.genoscope.cns.fr/Tetraodon.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1386 CTTCCGATCGTGTTCGACAGG 1408
|||||
Db 560 CTTCCGATCGTGTTCGACAGG 538

RESULT 2
AY105245 523 bp mRNA linear HTC 25-MAY-2002
LOCUS   Zea mays PC0098568 mRNA sequence.
DEFINITION
ACCESSION AY105245
VERSION AY105245.1 GI:21208323
KEYWORDS HTC.
SOURCE  Zea mays.
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 523)
AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
          Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
          Overgo Probes
JOURNAL   Unpublished (2002)
REFERENCE 2 (bases 1 to 523)
AUTHORS   Coe,E.C.
TITLE     Direct Submission
JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
          Missouri, Columbia, MO 65211, USA
FEATURES
  source
    1..523
      /organism="Zea mays"
      /db_xref="MaizeDB:635644"
      /db_xref="taxon:4577"
      /clone_lib="Maize Mapping Project/DuPont Consensus
      Library"
      /note="this sequence is part of a project of EST
      assemblies resulting from the application of public
      contigs to seed DuPont contigs; this resource was
      assembled by DuPont as part of a collaboration for the
      overgo addressing of BACs in conjunction with the Maize
      Mapping Project"
BASE COUNT 77 a 203 c 139 g 104 t
ORIGIN
Query Match 1.5%; Score 22; DB 11; Length 523;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CCCGTCGCCCGACGGCTTCC 61
|||||
Db 272 CCCGTCGCCCGACGGCTTCC 293

```

```

Db 167 CCCGTCGCCCGACGGCTTCC 188
|||||

RESULT 3
BH774999 530 bp DNA linear GSS 28-MAR-2002
LOCUS   fzmb011f004h06f0 fzmb filtered library Zea mays genomic clone
DEFINITION
ACCESSION BH774999
VERSION BH774999.1 GI:19777116
KEYWORDS GSS.
SOURCE  Zea mays.
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 530)
AUTHORS   Budiman,M.A., Freese,R.G., Bedell,J.A., Nunberg,A.N. and Lakey,N.D.
TITLE     Genethresher methylation filtered genomic sequences from maize
JOURNAL   Unpublished (2002)
COMMENT   Contact: Bedell JA
          Orion Genomics, LLC
          4041 Forest Park Ave, St. Louis, MO 63108, USA
          Tel: 314 615 6979
          Fax: 314 615 5975
          Email: jbedell@oriongenomics.com
          Plate: fzmb011f004 row: h column: 06
          Seq primer: M13 forward
          Class: shotgun
          High quality sequence stop: 530.
FEATURES
  source
    1..530
      /organism="Zea mays"
      /cultivar="M017"
      /clone_lib="fzmb011f004h06"
      /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
      prepared from purified nuclei was randomly sheared,
      end-repaired, size fractionated to enrich for the 0.5 to
      5 kb fraction, ligated into HincII-digested pBCSK(-)
      vector and electroporated into E. coli cells."
BASE COUNT 96 a 195 c 124 g 115 t
ORIGIN
Query Match 1.5%; Score 22; DB 17; Length 530;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CCCGTCGCCCGACGGCTTCC 61
|||||
Db 272 CCCGTCGCCCGACGGCTTCC 293
|||||

RESULT 4
AW231821 583 bp mRNA linear EST 30-MAR-2000
LOCUS   687042B12.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
DEFINITION
ACCESSION AW231821
VERSION AW231821.1 GI:6564199
KEYWORDS EST.
SOURCE  Zea mays.
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 583)
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
          University
JOURNAL   Unpublished (1999)

```

COMMENT

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 687042 row: B column: 12.
Location/Qualifiers

FEATURES

source
1. .583
/organism="Zea mays"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
/tissue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLF"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
; Site_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
2 others

BASE COUNT 85 a 218 c 175 g 103 t
ORIGIN
Query Match 1.5%; Score 22; DB 10; Length 583;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 CCCGTCGCGCGACGCTCC 61
|||||
Db 29 CCCGTCGCGCGACGCTCC 50

RESULT 5

AI102246/c
LOCUS AI102246 264 bp mRNA linear EST 31-JAN-1999
DEFINITION EST211535 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
RBC806 3' end, mRNA sequence.

ACCESSION AI102246
VERSION AI102246.1 GI:3707047
KEYWORDS EST.
SOURCE Rattus sp.

ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 264)
AUTHORS Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES

source
1. .264
/organism="Rattus sp."
/db_xref="ATCC (inhost):2024496"
/db_xref="taxon:10118"
/clone="RBC806"
/clone_lib="Normalized rat brain, Bento Soares"

BASE COUNT 72 a 55 c 71 g 66 t
ORIGIN
/note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"

Query Match 1.4%; Score 21; DB 9; Length 264;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 257 CGGCACCAACTTCTTCATCAA 237

RESULT 6

AI231258/c

LOCUS AI231258 322 bp mRNA linear EST 31-JAN-1999
DEFINITION EST27946 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMDE78 3' end, mRNA sequence.

ACCESSION AI231258
VERSION AI231258.1 GI:3815138
KEYWORDS EST.
SOURCE Rattus sp.

ORGANISM

Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 322)
AUTHORS Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES

source
1. .322
/organism="Rattus sp."
/db_xref="ATCC (inhost):2038867"
/db_xref="taxon:10118"
/clone="REMDE78"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
88 t

BASE COUNT 85 a 69 c 80 g 88 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 261 CGGCACCAACTTCTTCATCAA 241

RESULT 7

AI412412/c

LOCUS AI412412 341 bp mRNA linear EST 09-FEB-1999
DEFINITION EST240711 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
RBRDU52 3' end, mRNA sequence.

ACCESSION AI412412
VERSION AI412412.1 GI:4255916
KEYWORDS EST.
SOURCE Rattus sp.

ORGANISM

Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

```

REFERENCE
AUTHORS   Rattus...
          1 (bases 1 to 341)
          Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE      Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
          Gene Index
JOURNAL    Unpublished (1998)
COMMENT    Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
          Location/Qualifiers
            1..341
              /organism="Rattus sp."
              /db_xref="taxon:10118"
              /clone="RBRDU52"
              /note="lib="Normalized rat brain, Bento Soares"
              /note="Organ: brain; Vector: pT73Pac; Site_1: EcoRI;
              Site_2: NotI"
BASE COUNT      87 a 74 c 85 g 95 t
ORIGIN
Query Match      1.4%; Score 21; DB 9; Length 341;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
      |||||||
Db 257 CGGCACCAACTTCTTCATCAA 237

RESULT 8
AA899112/c
LOCUS      AA899112
DEFINITION UI-R-E0-cw-d-11-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone
           UI-R-E0-cw-d-11-0-UI 3' similar to gi|55891|emb|X54737|RNCBETAR Rat
           mRNA for the cystatin beta, mRNA sequence.
ACCESSION  AA899112
VERSION     AA899112.1 GI:4231612
KEYWORDS   EST.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE  1 (bases 1 to 371)
           Bonaldo,M.F., Lennon,G. and Soares,M.B.
           Normalization and subtraction: two approaches to facilitate gene
           discovery
JOURNAL    Genome Res. 6 (9), 791-806 (1996)
MEDLINE    9704477
COMMENT    On Apr 7, 1998 this sequence version replaced gi:3034466.
           Contact: Soares, MB
           Program for Rat Gene Discovery and Mapping
           University of Iowa
           451 Eckstein Medical Research Building Iowa City, IA 52242, USA
           Tel: 319 335 8250
           Fax: 319 335 9565
           Email: msoares@blue.weeg.uiowa.edu
           The sequence tag present in the cDNA between the NotI site and the
           oligo-dr track served to identify it as a clone from the normalized
           adult 8-day-Embryo library. cDNA Library Preparation: M. Fatima
           Bonaldo, Ph.D. Clone distribution: clones will be available through
           Research Genetics
           Seq primer: M13 Forward.
           Location/Qualifiers
            1..371
              /organism="Rattus norvegicus"
              /strain="Sprague-Dawley"
              /db_xref="taxon:10116"

```

```

/clone="UI-R-E0-cw-d-11-0-UI"
/dev_stage="embryonic"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73b-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; This library
consists of a mixture of individually tagged normalized
libraries constructed from 8, 12 and 18-day embryo. The
tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dr track which allows
identification of the library of origin of a clone within
the mixture."
BASE COUNT      103 a 72 c 85 g 111 t
ORIGIN
Query Match      1.4%; Score 21; DB 9; Length 371;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
      |||||||
Db 352 CGGCACCAACTTCTTCATCAA 332

RESULT 9
AI409646/c
LOCUS      AI409646
DEFINITION EST237938 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
           ROVEN88 3' end, mRNA sequence.
ACCESSION  AI409646
VERSION     AI409646.1 GI:4253150
KEYWORDS   EST.
SOURCE     Rattus sp.
ORGANISM   Rattus sp.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE  1 (bases 1 to 374)
           Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
           Kerlavage,A.R. and Adams,M.D.
           Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
           Gene Index
JOURNAL    Unpublished (1998)
COMMENT    Contact: Lee, NH
           The Institute for Genomic Research
           9712, Medical Center Drive, Rockville, MD 20850, USA
           Tel: (301)-838-3529
           Fax: (301)-838-0208
           Email: nhlee@tigr.org
           Seq primer: M13-21.
           Location/Qualifiers
            1..374
              /organism="Rattus sp."
              /db_xref="taxon:10118"
              /clone="ROVEN88"
              /note="lib="Normalized rat ovary, Bento Soares"
              /note="Organ: ovary; Vector: pT73Pac; Site_1: EcoRI;
              Site_2: NotI"
BASE COUNT      110 a 70 c 92 g 102 t
ORIGIN
Query Match      1.4%; Score 21; DB 9; Length 374;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
      |||||||
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 10
AI234086/c
LOCUS      AI234086

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DEFINITION EST230774 Normalized rat lung, Bento Soares Rattus sp. cDNA clone
ACCESSION RLUC095 3' end, mRNA sequence.
VERSION AI234086
KEYWORDS EST.
SOURCE AI234086.1 GI:3817966
ORGANISM Rattus sp.
          Rattus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 381)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
          Gene Index
JOURNAL Unpublished (1998)
COMMENT Other ESTs: TC62051
          Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
          Location/Qualifiers
            1..381
              /organism="Rattus sp."
              /db_xref="ATCC (inhost):2039745"
              /db_xref="taxon:10118"
              /clone="RLUC095"
              /clone_lib="Normalized rat lung, Bento Soares"
              /note="Organ: lung; Vector: pT7T3Pac; Site_1: EcoRI;
              Site_2: NotI"
BASE COUNT 114 a 73 c 91 g 103 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 381;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 11
AI179240/c
LOCUS AI179240
DEFINITION EST22931 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
ACCESSION RSPCE16 3' end, mRNA sequence.
VERSION AI179240
KEYWORDS EST.
SOURCE AI179240.1 GI:3729878
ORGANISM Rattus sp.
          Rattus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 392)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
          Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
          Location/Qualifiers
            1..392
              /organism="Rattus sp."
              /db_xref="ATCC (inhost):2039745"
              /db_xref="taxon:10118"
              /clone="RSPCE16"
              /clone_lib="Normalized rat spleen, Bento Soares"
              /dev_stage="embryo 8, 12, 18 dpc"
              /note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 117 a 76 c 93 g 111 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 13
AW141507
LOCUS AW141507
DEFINITION EST291561 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
          RIBX21 5' end similar to cystatin beta, mRNA sequence.
ACCESSION AW141507
VERSION AW141507.1 GI:6161305
          Location/Qualifiers
            1..392

```

```

/organism="Rattus sp."
/db_xref="ATCC (inhost):203816"
/db_xref="taxon:10118"
/clone="RSPCE16"
/clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 30 a 91 c 105 g 106 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 257 CGGCACCAACTTCTTCATCAA 237

RESULT 12
AI103006/c
LOCUS AI103006
DEFINITION EST212295 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
          REMBW03 3' end, mRNA sequence.
ACCESSION AI103006
VERSION AI103006.1 GI:3704801
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
          Rattus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 397)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
          Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.
          Location/Qualifiers
            1..397
              /organism="Rattus sp."
              /db_xref="ATCC (inhost):2023069"
              /db_xref="taxon:10118"
              /clone="REBW03"
              /clone_lib="Normalized rat embryo, Bento Soares"
              /dev_stage="embryo 8, 12, 18 dpc"
              /note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 117 a 76 c 93 g 111 t
ORIGIN
Query Match 1.4%; Score 21; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 CGGCACCAACTTCTTCATCAA 1019
|||||
Db 337 CGGCACCAACTTCTTCATCAA 317

RESULT 13
AW141507
LOCUS AW141507
DEFINITION EST291561 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
          RIBX21 5' end similar to cystatin beta, mRNA sequence.
ACCESSION AW141507
VERSION AW141507.1 GI:6161305
          Location/Qualifiers
            1..392

```

KEYWORDS
SOURCE
ORGANISM

EST.
Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 399)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
Unpublished (1998)
Contact: Lee, NH

JOURNAL
COMMENT

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For information availability, additional sequence and expression
information related to this EST please check the TIGR Rat Gene
Index (<http://www.tigr.org/tdb/rgi/rgi.html>). To order a clone
contact the ATCC (<http://www.atcc.org/atcc.html>).
Seq primer: M13 Reverse.

FEATURES
source

Location/Qualifiers
1..399
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGIBX21"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT73pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 110 a 104 c 94 g 91 t

Query Match 1.4%; Score 21; DB 10; Length 399;

Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CGGCACCAACTTCTTCATCAA 1019

Db 150 CGGCACCAACTTCTTCATCAA 170

RESULT 14

BE110478/c
LOCUS
DEFINITION BE110478 401 bp mRNA linear EST 13-JUN-2000
UI-R-BJ1-auc-e-03-0-UI-s1 UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-auc-e-03-0-UI 3', mRNA sequence.

ACCESSION BE110478

VERSION BE110478.1 GI:8502583

KEYWORDS EST.

SOURCE

ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 401)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL
MEDLINE

COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site

FEATURES

source

Location/Qualifiers
1..401
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ1-auc-e-03-0-UI"
/clone_lib="UI-R-BJ1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73d-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1
library is a subtracted library derived from the following
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV
canal at 15 dpc, ventricle at 13 dpc, and adult heart.
For a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-BJ1
TAG_TISSUE=AV canal at 16.5 dpc
TAG_SEQ=GAACC"
BASE COUNT 115 a 72 c 92 g 122 t

Query Match 1.4%; Score 21; DB 10; Length 401;

Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CGGCACCAACTTCTTCATCAA 1019

Db 354 CGGCACCAACTTCTTCATCAA 334

RESULT 15

BG371835/c
LOCUS
DEFINITION BG371835 401 bp mRNA linear EST 09-MAR-2001
UI-R-CV0-bri-h-07-0-UI-s1 UI-R-CV0 Rattus norvegicus cDNA clone
UI-R-CV0-bri-h-07-0-UI 3', mRNA sequence.

ACCESSION BG371835

VERSION BG371835.1 GI:13268372

KEYWORDS EST.

SOURCE

ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 401)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL
MEDLINE

COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dr track served to verify it as a clone from the
non-normalized rat eye library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through

and the oligo-dr track served to identify it as a clone from the
normalized AV canal at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes.

Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes

FEATURES
source
Location/Qualifiers
1..401
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CV0-bri-h-07-0-UI"
/clone_lib="UI-R-CV0"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT3D-pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-CV0
library is a non-normalized library constructed from rat
eye tissue. For a detailed description of the library from
which this clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG.LIB=UI-R-CV0
TAG.TISSUE=rat eye
TAG_SEQ=CAGCC"

BASE COUNT 115 a 73 c 91 g 122 t
ORIGIN

Query Match 1.4%; Score 21; DB 12; Length 401;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 999 CGGCACCACTTCTTCATCAA 1019
|||||
Db 355 CGGCACCACTTCTTCATCAA 335

Search completed: December 14, 2002, 08:22:39
Job time : 2155 secs

RESULT 5

US-09-732-350-5
; Sequence 5, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20010031490A1 No. US20010031490A1disk of No. US20010031490A1alt
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,350
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,315
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-732-350-5

Query Match 44.2%; Score 1178.5; DB 10; Length 529;
Best Local Similarity 47.4%; Pred. No. 9.6e-91;
Matches 243; Conservative 66; Mismatches 159; Indels 45; Gaps 12;

Qy	10	VANAPVSPDGLRDAIVVNGVPSPLITGKGRFQNLNVVDLTNNHMLKSTSIHHGFF	69
Db	29	IKNVNAPDGFQRSIVSNGVLPGTLITANKGDTLRINVTNQLTDPMSRRATTIHHGLF	88
Qy	70	QAGTNWADGPAFVNOCPASGHSFLYDFHVPDQAGTWTYHSHLSQYCDGLRGPFVYDP	129
Db	89	QATTADEGPAFVTCQPIAQNLSYETPLRGQTGTWYHAHLASQYVDGLRGPLVIYDP	148
Qy	130	KDPHASRYDVNDSVTITLDWYHT-----AALRGPRPLGADATLINGL	175
Db	149	NDPHKSRVDVDDASTVWLEMDYHTTAPVLEKQMFSTNTALLSP-----VPDGLINGKG	204
Qy	176	RSASTPTAALAVINQHGKRYRFLVISCDPNTFTSIDGHNLTIVIEVDGINSQPLIVDS	235
Db	205	RYVGGPAVPRSVINVKRGKRYRLRVINASAIGSTFSEIHSLSVIEADGILHQLAVDS	264
Qy	236	IQIFAAQRYSVFLNQTGVNWRPNFTGVCFAGGINS-----AIIRYGAPVAEPTT	291
Db	265	FQIVAGORYSIVEANQTAANYWIRAPMTVAGAGTANALDPTNVFVFLHYECAPNAEPTT	324
Qy	292	TQTTSTV-IPLITNLHLPLAMPVPGSPPTPGVDKALNLAFFNGTIN-----FFFINNATFT	346
Db	325	EGGSAIGTALVEENLHALINFGAGGSGAP--ADVSLNLAIGRSIVDGLITRTFNKIKYA	382

Qy	347	PTVPVLQIL-SGAQTAODLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLGHAF	405
Db	383	PSLPTLLKLIANNASNDADFTNEHTIVLPHNKVIELNITG-----GADHPILHGHVFD	437
Qy	406	VYRSAGSTTYNYNDPIFRDVSVTGTGPAAGDNVTIRFQTDNPGFWFHLCHIDHLDAGFAI	465
Db	438	IVKSLGGTP-NYVNPERRDVRVG-----GTGVVLRKFTDNPFGWFWHCHIDHLEAGLAL	492
Qy	466	VFAEDVAD-----VKAANPVPKAWSDLCPYDGL	494
Db	493	VFAEAPSQIROGVQSVQP-NNAMNOLCPKYAAL	524

RESULT 6

US-09-732-350-6
; Sequence 6, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20010031490A1 No. US20010031490A1disk of No. US20010031490A1

CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,350
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/032,315
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-732-350-6

Query Match 37.5%; Score 1000; DB 10; Length 599;
Best Local Similarity 38.7%; Pred. No. 9e-76;
Matches 226; Conservative 72; Mismatches 180; Indels 106; Gaps 14;

Qy	10	VANAPVSPDGLRDAIVVNGVPSPLITGKGRFQNLNVVDLTNNHMLKSTSIHHGFF	69
Db	28	VANGAVAPDGVTRNAVLRNGRFGPLITANKGDTLRKLNKLSDPTRRRSTTIHHGGL	87
Qy	70	QAGTNWADGPAFVNOCPASGHSFLYDFHVPDQAGTWTYHSHLSQYCDGLRGPFVYDP	129
Db	88	QHTAEEDGPAFVTCQPIPPQESTYTPMPLGEQGTWYHSHLSQYVDGLRGPIVIYDP	147
Qy	130	KDPHASRYDVNDSVTITLDWYHTAARLGRPRPLGA-----DATLINGLR-----	176
Db	148	HDPRNRYVDVDDTERTVTLADWYHT-----PSEAIATHDVLKTPDSGTINGKGYDPA	202


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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-732-350-8

Query Match 33.1%; Score 884.5; DB 10; Length 575;
Best Local Similarity 37.5%; Pred. No. 3.7e-66;
Matches 211; Conservative 79; Mismatches 184; Indels 89; Gaps 19;

QY 8 LVANAPVSPDGLRDAIVGVVPSPLITGKGRFOLNVDTLTNHSMLKSTSIHHWG 67
Db 26 LKISDGEIADPGVKRNATLVGGYPCGLIFANKGDTLKVQVQKLTNPENYRTTSIHHG 85
QY 68 FFOAGTNWADGPAFVNOCPASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPFVY 127
Db 86 LLQHRNADDGSPSVTCPIVPRESYTYTIPDDQGTWYHSHLSQYVDGLRGLVIY 145
QY 128 DPDPHASRYDVNDNESTVITLTDMYHTAA-----LGRFPLGADATLNLGSRAS 180
Db 146 -PKDPHRLDYDDEKTVLIGDWHYESSKAILASGNITRQRPVSA---TINGKRPDPD 201
QY 181 PTAA----LAVINVQHGKRYRFLVLSVSCDPNYTFSDGHNLTVIEVDGINSOPLVDSI 236
Db 202 NTPANPDTLTLYKVRGKRYRLRVINSEIASFRSEVGHKVTVIAADGVSTKPYQVDAF 261
QY 237 QIFAAQYSFVLNQTGVNYYVRAN---PNFGTVGF-----AGGI 274
Db 262 DILAGQRIDCVANQEPDIYWINAPLTNPVNTKAQALLVYEDRRPYHPKGYRQWSV 321
QY 275 NSAILRYOG-----APVAEPT-----TTQTSVPIPLIETNLH 306
Db 322 SEAIKYWNHKKHGRGILLGSHGGLKARMIEGSHLHRSRVKVRQNETTVV-MDESKLV 380
QY 307 PLARMPVPGSTPG-GVDKALNLAF--NENGTFEINNATFTPTVPVLLQLLSGAQ--T 361
Db 381 PL---EYPGAACGSKPADVLVDLTFLGLNFATGHWINGIPYESKPIPTLLKILDEGVT 437
QY 362 AQDLLPAGSVYPLPAHSTIETTLPTALAPGAPHPFHLGHAFVAVRSAGSTTYNYNDPI 421
Db 438 ESDFTKEHTVILPKNKCIEFNKNSGIP-ITHPVHLGHTWDVQ-FGNPNPNYVNP 495
QY 422 PRDVVGTGTPAAGNVITRFOTDNPDPWFHLCHIDFHLADGAFALVFAEDVADVKAANVP 481
Db 496 RRDVV--GSTDAG--VRIQFTDNPDPWFHLCHIDHWHLEGFAMVFAEPAVKGG---P 548
QY 482 KA-----WSDLCPIYDGLSEAN 498
Db 549 KSAVDSQWEGLCCKYDNWLSKN 571

RESULT 9
US-09-732-350-9
; Sequence 9, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. US20010031490A1o No. US20010031490A1disk of No. US20010031490A11th
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; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,350
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/032,315
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-732-350-9

Query Match 21.6%; Score 577; DB 10; Length 616;
Best Local Similarity 29.5%; Pred. No. 1.9e-40;
Matches 160; Conservative 82; Mismatches 199; Indels 102; Gaps 21;

QY 10 VANAPVSPDGLRDAI-VVNGVVPSPPLITGKGRFOLNVDTLTNHSMLKSTSIHHWG 68
Db 89 VDNRP-GPDGVKEKMLINDKLLGPTVFANWGTIEV---TVNNHLRTNGTSHHGL 143
QY 69 FQAGTNWADGPAFVNOCPASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPFVYD 128
Db 144 HQGTNYHDGANGVTECPPIPGGSRVYSFRA-ROYGTSWYHSHFSAQYGVGSGAIQI-- 200
QY 129 PKDPHASRYDVNDNESTVITLTDMYHTAA-----RLGPRFPLGADATLNLGSRAS 182
Db 201 -NGPASLPYDID--LGVLPLXDMWYKSADQVLTLLKGNAPFSDNYLNGTAKHPPTGE 257
QY 183 AALAVINVQHGKRYRFLVLSVSCDPNYTFSDGHNLTVIEVDGINSOPLVDSIQIFAAQ 242
Db 258 GEVAIVKLTDPKRRHLRLINNSVENHFQVSLAKHTMTVIAADMVVPVNAVTDSLMAVGQ 317
QY 243 RYSFVLNANQTGVNYYVRANPEG---TVGFA-GGINSAILRYOGAPVAEPT----- 290
Db 318 RYDVTIDASQAVGYWF--NITFGGQOKCGFSHNPAPAAIFRYEGADALPTDPGAAPKD 375
QY 291 --TQTTTSVPIETNLHPLARMEVPGS--PTPGGVDPKALN---LAFNFGT----- 335
Db 376 HQCLDTLDSLPPVQKNVPVDGFYKEPGNTLPVTLHVDOAAAAPHVFTWKINGSAADVDWR 435
QY 336 ---NFFINNATFTPTVPVLLQLLSGAQTAQDILL---PAGSVYPLPAHSTIETLPTAL 389
Db 436 PVLEYVMNNDLSSIPVKNVVRVDGVNWTWLVLENDPEGLR-----NDPIRDRVSTGPA 477
QY 390 APGAPHFHLGHAFV-----VRSAGSTYNY-----NDPIRDRVSTGPA 432
Db 478 --SLPHPMHLGHCHDFVILGRSPDVSPDSETRFVDFDPAVDLPRLRGHAPVRDVTMLPA 533
QY 433 AGDNVITRFOTDNPDPWFHLCHIDFHLADGAFALVFAEDVADVKA-----ANPVPKA 483
Db 534 RG-WLLAFRTDNFGANLFFCHIXAHXVSGGLSVDFLERPDELRLQLTGESKALERVCRE 592
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QY 484 WSD 486
Db 593 WSD 595

RESULT 10
US-09-732-350-10
; Sequence 10, Application US/09732350
; Patent No. US20010031490A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. US20010031490A1o No. US20010031490A1disk of No. US20010031490A1th
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09732.350
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/032.315
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-732-350-10

Query Match 21.5%; Score 575; DB 10; Length 573;
Best Local Similarity 29.9%; Pred. No. 2.5e-40;
Matches 163; Conservative 74; Mismatches 200; Indels 108; Gaps 22;

QY 17 PDGFLRDAI-VYNGVVPPLITGKGRFQNLNVVDTLTNHSMKSTSIHHWGHFFOAGTNW 75
Db 49 PDGVVKEKVMVNLNSIGTFADWDGTIOQVIVNNLETN----CTSIHHGLHKGQNL 104
QY 76 ADGPFAVNOCPIT-ASGHSELYDFHVPDQAGTFWYHSHLSTQYCDGLRGPFFVYDPKDPHA 134
Db 105 HDGANGITECPPIPPGGRKVRFRKA-QQYGTSWYHSHFSAQYGNVGWGAIQI---NGPAS 160
QY 135 SRYVDNESTVITLTDWHTAA-----RLGPRFLGADATLNLGLRSASTPTAALA 186
Db 161 LPYDID--LGVPISDYISSADELVELTKNSGAPF---SONLFGAKHPETEGEYVA 215
QY 187 VINOHGKRYRPLVSIKCDPNYTFSDIHNLTIVIEVDGINSQPLLVDISIQIFAAQRYSF 246
Db 216 NVTLTPGRRHRLRLNTSVENHFQVSLVNHTMCIIADWVPVNMATVDSLFLGVGQRYDV 275
QY 247 VLNAQNTGVNWRANPNFGVGFAGGIN-----SAILRYQGAQPAEPTTQTTSV----- 297
Db 276 VIEANRTPGNWF--NVTFGGLLCGGRNPNYPPIAFHYAGPGPGPTDEKAPVDHNC 333

QY 298 -IPLIETNHLHLPMPVPGSPTPGGVDKALNLAENFNGTNEF---INNATFTPTPTVPLL 353
Db 334 DLP----HLKPVVARDVPLSGFAKRADNTLDVTLDTGTPLEFWKVNLSA-----I 380
QY 354 QILSGAQTAQDILLPAGSVYPLPAHSTIET-----TLPATALAPGA-----PHPFHLHGH 403
Db 381 NIDWGRAVVDYVLTQNTSFP-PGYNIVEVNGADQWSYLIENDPGAPFTLPHPMHLGH 439
QY 404 FAVV-----RSAGSTTYNYNDPIFRDVTSTGTPAAGDNWTTIRFQTD 444
Db 440 FYVLGRSPDESPASNERHVFDPARDAG--LLSGANPVRDV--SMLPAFG-WVVLISFRAD 494
QY 445 NPGPWFILCHIDFHLDAQFAIVFAEDVADVKAA-----NPVPK 482
Db 495 NPGAWLFIHCHIAHWVSGGLGVVYLERADDLRGAVSDADADDLRLCADWRRITWNTNPK 554
QY 483 AWSDL 487
Db 555 SDSGL 559

RESULT 11
US-09-944-160-12
; Sequence 12, Application US/09944160
; Patent No. US20020174452A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, No. US20020174452Alman
; APPLICANT: Davin, Laurence
; APPLICANT: .. Huang, Ning
; TITLE OF INVENTION: Monocot
; FILE OF INVENTION: Content
; FILE REFERENCE: WSUR117983
; CURRENT APPLICATION NUMBER: US/09/944.160
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/230.632
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: laccase amino acid sequence from plasmid PAP1245
US-09-944-160-12

Query Match 19.2%; Score 512.5; DB 9; Length 564;
Best Local Similarity 28.3%; Pred. No. 4.1e-35;
Matches 149; Conservative 72; Mismatches 224; Indels 81; Gaps 16;

QY 22 RDAIVVNVVSPSLITGKGRFQNLNVVDTLTNHSMKSTSIHHWGHFFOAGTNWADGPAF 81
Db 46 KSIFVNVNQFPGPTIYATEGDTI---IVDVINQPS--ENVTIHWHGVKOPRYPWSDGPY 100
QY 82 VNOCPIAGSHSELYDFHVPDQAGTFWYHSHLSTQYCDGLRGPFFVYDPKDPHASRYDV 141
Db 101 ITQCFIQGANFSQKIIISDEIGTLWHAHSDWSRAT-VHGAIVIRPKNNSNYPFTTDA 159
QY 142 ESTVITLTDWHTAARLGRPRPLG-----ADATLING-----LGRSASTPTAALAVIN 190
Db 160 EATII-LGEWKSIDIRAVQNEFLNGGDGANYSDAFLINGPCDGLYPCSRSDTYNL---TV 215
QY 191 QHGKRYRPLVSIKCDPNYTFSDIHNLTIVIEVDGINSQPLLVDISIQIFAAQRYSFV 250
Db 216 ESGTYLRIRMINAVMNTIMFFSIANHSVTVVGSDAAATKPLKSDYITISPGOTIDFLQA 275
QY 251 NOTGVNRYKVRANPNFGTVGFAGGINSAILRYQGAQPAEPTTQTTSVLIETN----- 304
Db 276 NOTPSHYMAARAVAVAGNFNTTTTALIRKGNVTA-PPSPSPFNLPGLCFNDTNASVFT 334
QY 305 --LHPLAMPVPGSPTPGGVDKALNLAENFNGT-----NFFINNTATFTTP 347
Db 335 YLRSLGNKNYP-VDPKPNVTDKLLFTFSINLTPCPNNSCAGPFRFRASVNNITFVPP 393
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:14:26 ; Search time 66 Seconds

(without alignments)

8987.750 Million cell updates/sec

Title: US-09-786-960-1

Perfect score: 1500

Sequence: 1 gccatcgccggtgagcag.....tgagcagggtaccagtga 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/FCIUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	56.6	3.8	1965	10	US-09-826-660-26
2	54.6	3.6	88421	9	US-09-976-059-1
3	53.2	3.5	88421	9	US-09-976-059-1
4	50.2	3.3	1722	9	US-09-938-842A-1675
5	47.4	3.2	1488	10	US-09-764-870-209
6	47.4	3.2	2531	10	US-09-764-870-49
7	47.2	3.1	1713	9	US-09-938-842A-1910
8	46.8	3.1	5036	10	US-09-918-951-2
9	46.2	3.1	2010	12	US-10-032-717-9
10	46.2	3.1	2838	10	US-09-954-456-700
11	46.2	3.1	2838	10	US-09-954-456-966
12	46.2	3.1	2838	10	US-09-954-456-1143
13	44.8	3.0	1395	10	US-09-815-242-4093
14	44.2	2.9	2155	10	US-09-962-436-299
15	44.2	2.9	2155	10	US-09-880-107-2394
16	44.2	2.9	6200	9	US-09-993-241-1
17	44.2	2.9	6200	10	US-09-993-038-1
18	43.6	2.9	2163	10	US-09-939-408A-29
19	43.2	2.9	1248	9	US-09-860-846-7

20	43.2	2.9	1248	10	US-09-861-289-7
c 21	43.2	2.9	13613	9	US-09-860-846-3
c 22	43.2	2.9	13613	10	US-09-861-289-3
23	42.8	2.9	2430	9	US-09-860-846-23
24	42.8	2.9	2430	10	US-09-861-289-23
25	42.8	2.9	4689	9	US-09-860-846-34
26	42.8	2.9	4689	10	US-09-861-289-34
27	42.8	2.9	13613	9	US-09-860-846-3
28	42.8	2.9	13613	10	US-09-861-289-3
29	42.8	2.9	36778	9	US-09-860-846-5
30	42.8	2.9	36778	10	US-09-861-289-5
31	42.4	2.8	2322	10	US-09-476-242-18
32	42.4	2.8	2322	10	US-09-476-242-19
33	42.4	2.8	2322	10	US-09-476-242-20
34	42.4	2.8	2322	10	US-09-476-242-7
35	42.2	2.8	1140	9	US-09-860-846-15
36	42.2	2.8	1140	10	US-09-861-289-15
37	42.2	2.8	1296	10	US-09-815-242-4090
38	42.2	2.8	2712	10	US-09-748-033-4
39	42	2.8	1375	10	US-09-770-621-1
40	41.4	2.8	491	10	US-09-833-790-353
41	41.4	2.8	1107	10	US-09-748-033-6
42	41.2	2.7	424	10	US-09-960-352-12392
43	41.2	2.7	788	9	US-10-076-785-55
44	41.2	2.7	2310	10	US-09-476-242-3
45	41	2.7	3189	10	US-09-815-242-4056

ALIGNMENTS

RESULT 1

US-09-826-660-26
; Sequence 26, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-26

Query Match	3.8%;	Score 56.6;	DB 10;	Length 1965;
Best Local Similarity	44.1%;	Pred. No. 6e-05;		
Matches	331;	Conservative	0;	Mismatches 414;
				Indels 6;
				Gaps 2;
QY	669	CGACGGTATCAACAGCAGCGCTCTCCTGTGACCTATCCAGATCTTCGCCGCGGACGC	728	
Db	1185	CGCGCAGGATCACCTCCACACCGCGCTCTTCAACACCAACCGCGCGGCGCATCGA	1244	
QY	729	CTACTCCTTTGTTGTTGAATGCGAACCAACGGTCGGGAACCTACTGGTCCGCGGACCC	788	
Db	1245	CTCAGGGGCGCGCAATTTCCGGCAACCTCTACGCCACCTCTACGGGTGTCTCTCCCTCAA	1304	
QY	789	GRACCTCGGACGGTTGGTTCGCCGGGGGATCACTCGGCCATCTTGGCTACCAAGG	848	


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; NAME/KEY: misc_feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; NAME/KEY: misc_feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (84481)..(85548)
; OTHER INFORMATION: ORF 30; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1

Query Match          3.6%; Score 54.6; DB 9; Length 88421;
Best Local Similarity 46.6%; Pred. No. 0.00049;
Matches 174; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 1116 CCGCTCCCGCCGCTCCACCATCGATCAGCTGCGCCGCGACCGCTTGCCCGCGG 1175
    ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47206 CCGCGTTCGGCGAGTTTCGACCTCGACCTCAGCTTACCGAGACCTTCGAGCGCGGG 47265
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1176 TGCACCGCACCCCTTCACCTCAGCGCTCAGCGCTTCGCGGTCGTTTCGAGCGCGGGAG 1235
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47266 GGAGCGCGCGCGCTCGCGTTCGACCTCATCGGGCGCGGACCTTTCGAGCGCGGGAC 47325
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1236 CACCGAGTATACTAACAGACCCGATCTCCGCGAGCTGTGAGCAGCGCGACCGCCGC 1295
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47326 GCGCGCGCGCGCTCGCGGTACCTGAGCGCGCTTCTCGCGCTGCTCGCGCGATCCGCG 47385
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1296 CCGCGCGCAACAGTCCAGCATCGCTTCCAGAGCAACCCCGCGCGCTGCTCTCCA 1355
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47386 GCGCGCGCTGCGGAGTCCAGCGCTGAGCGGAGGAGCGCGCTCATGCTCCCGCG 47445
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1356 CTGCCACATCGACTTCCACCTTCGACCGCGGCTTCGCGATCGTGTTCGAGAGGACGTTGC 1415
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47446 CCGTGAGGAGCGCGCGCGCGCTGCCGAGATCACCGTCCGCGCGCTCGTCCCGAGCA 47505
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1416 GGACGTGAGGCGCGCAACCCGTTCCGAGCGGTGTCGACCTGTCGCCGATCTACGA 1475
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47506 GTGCGCGCGCGAGCGCGGTCGCGTCCGCGTCCGAGCGCGAGCGCGGAGCTGACCTACGC 47565
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1476 CCGGCTGAGCGAG 1488
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DB 47566 CGAGCTCGAGAG 47578

RESULT 3
US-09-976-059-1/c
; Sequence 1, Application US/09976059
; Patent No. US20020164747A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
; FILE REFERENCE: 3019-PCT
; CURRENT APPLICATION NUMBER: US/09/976,059
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; FEATURE:
; NAME/KEY: misc_feature
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OTHER INFORMATION: ORF 24; negative strandedness
NAME/KEY: misc_feature
LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25; negative strandedness
NAME/KEY: misc_feature
LOCATION: (81624)..(79861)
OTHER INFORMATION: ORF 26; negative strandedness
NAME/KEY: misc_feature
LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27; negative strandedness
NAME/KEY: misc_feature
LOCATION: (82346)..(82062)
OTHER INFORMATION: ORF 28; negative strandedness
NAME/KEY: misc_feature
LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 29; positive strandedness
NAME/KEY: misc_feature
LOCATION: (84481)..(85548)
OTHER INFORMATION: ORF 30; positive strandedness
NAME/KEY: misc_feature
LOCATION: (85556)..(86845)
OTHER INFORMATION: ORF 31; positive strandedness
NAME/KEY: misc_feature
LOCATION: (87372)..(86803)
OTHER INFORMATION: ORF 32; positive strandedness
NAME/KEY: misc_feature
LOCATION: (87494)..(88420)
OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1

Query Match 3.5%; Score 53.2; DB 9; Length 88421;
Best Local Similarity 54.0%; Pred. No. 0.0011;
Matches 109; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 1281 CACGGGACGCGCGCGCGGACGATCCAGTCACGCTTCCAGCAGGACACCCCGG 1340
DB 74244 CCCTGCCCAACCGGAGGAGGACGATGACGCTCGTCTGATCGCGCAGATCA 74185
QY 1341 GCCGTGTTCTCCACATGACATGACCTCCAGCTCGACCGGGCTTCGGGATCGTGT 1400
DB 74184 GCGATGATCGGAGTGGCTTGGCTGATCTCGAGGAGCGCGGATCGAGGTGT 74125
QY 1401 GCGAGAGACGTTGGGAGGAGGCGGAGACCCGTTCCGAGGCGGTGCGGACCT 1460
DB 74124 GCGGAGGCGGCTGACGCGGTGGAGCGGTGCGACAGGCGGCAAGCTGCGCGGAGGT 74065
QY 1461 GTGCCGATCTACGACGGGTG 1482
DB 74064 GTGCTGTGGACATCCGCATG 74043

RESULT 4
US-09-938-842A-1675
Sequence 1675, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRI1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1675

LENGTH: 1722
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1675
Query Match 3.3%; Score 50.2; DB 9; Length 1722;
Best Local Similarity 52.5%; Pred. No. 0.0021;
Matches 134; Conservative 0; Mismatches 118; Indels 3; Gaps 1;
QY 138 CACGTCGTGACACCTTGACCAACACACAGCATCTCAAGTCCACTAGTATCCACTGGCA 197
DB 186 CACGTCATTTATCCAGCTGTCACAAACTCTCCACCAAGGTGTTGTTATCCATTGGCA 245
QY 198 CGGCTTCTCCAGGACGACCAACTGGGACAGACCCCGCTTCGTCACACCAAGTCCGC 257
DB 246 CGGCATACGTCAGAAAGGAGCTCCATCGGCTGATGGAGCAGCAGGTGTGACCCAGTGCC 305
QY 258 TATTGCTTCGGGCAATTCATTTCTGTAGGACTTCCATGTGCCGACGAGGACGAGTGT 317
DB 306 TATTAATCCTGGCGAGACTTTTCACTTACAGTTCAATTGT---CGATAAGCGGGGACACA 362
QY 318 CTGCTACACAGTCATCTGTCTACGCAATACTGTGACGGGCTGCGAGGACGTTTCGTGCT 377
DB 363 TTTCTACATGGACACTACGGAATGCAAGATCATCGGGACTATACGAATGTTAATAGT 422
QY 378 GTACGACCCCAAGGA 392
DB 423 AAGATCACCAAAAGA 437
RESULT 5
US-09-764-870-209
Sequence 209, Application US/09764870
Patent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 209
LENGTH: 1488
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1461)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1467)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1473)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (1482)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-870-209
Query Match 3.2%; Score 47.4; DB 10; Length 1488;
Best Local Similarity 50.7%; Pred. No. 0.0099;
Matches 114; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
QY 1185 CCCCTTCCACCTGCACGCTCAGCGCTTCGCGTTCGTCAGCGCGGAGGACACACGTA 1244
DB 306 CCCCTACACGCTGAACGCTTACGCGCTGCGCTGACTCCGCTCGGAGAGATCATCCACA 365
QY 1245 TAACTACAACGACCGCATCTTCCGCGAGCTGTGAGCAGCGACGCGCGCGCGGCGGA 1304
DB 366 CTACGACAGTGACAAGATGTTCCCTGCGCTTCCGCGGCTTCCGCGGACGCTGCCCGGATGG 425

Db 649 CACCAGACCCGTCCTCAATACCTAACCCAGCACCACCAACCTGAGCGCGACCTCGGCTCAA 590
QY 1062 GATTCGAGCGTGGCAGACCGCACAAGACCTGCTCCCTGCAGGCTCTGTCTACCCGCT 1121
Db 589 TCACGGCAGTAACACCCAGACGACCTGGCAGCACAAGCGACCTGAGCGCGGAAACAC 530
QY 1122 CCCGGCCACTCCACATCGAGATCAGCTGCGCCGCGACCGCTTGGCCCGGGTGCACC 1181
Db 529 CGCTTGACGGCGAGAGCCAGCCACCTGACCAGGACCCAGCACCAGCCAGTCGGTAG 470
QY 1182 GCACCCCTTCCACCTGCAGCGTCAGCCCTTCGCGGTGCTGCGACGCGGGGAGACAC 1241
Db 469 CCAGGCGCCGACCGACATCGCTGCTGATGACGCTTGCACACCCCGCGCGCTCACGG 410
QY 1242 GTATACTACACGACCCGATCTTCGGCAGCTGCTGAGCAGGCG 1287
Db 409 CGAAGCGGACATGGCGAGCTCTCGCAAGCCCATGGCGAGCGGC 364

RESULT 9

US-10-032-717-9
; Sequence 9, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Peng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; OTHER INFORMATION: Maize optimized Cry1218-1
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: mo1218-1
US-10-032-717-9

Query Match 3.1%; Score 46.2; DB 12; Length 2010;
Best Local Similarity 49.8%; Pred. No. 0.021;
Matches 117; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY 1161 CGCCTTGGCCCGGGTGCAACCGACCCCTTCCACCTGCAGGTCAGCCCTTCGCGGTGCT 1220
Db 882 CCCCATGGAGAACCAAGCGCCAGCTACCGCGAGGTGTACACGACCCCGCTCGCGCGCT 941
QY 1221 TCGCAGCGCGGGAGCACCACGCTATTAACACAGCAGCCGATCTTCGGGACGTCGTGAG 1280
Db 942 GAACGTGTCTCTCGCTGGCTTGGTACGACAAAGGCCCAAGCTTCGGGTGTATCGATC 1001
QY 1281 CACGGGACACCGCGCGCGGCGACACAGTCACGATCCGCTTCCAGACGGACAAACCCGG 1340
Db 1002 CTCGCTGATCCGCGCGCGCACTGTTCGACTACATCACCGGCTTCACCGTGTACACCCA 1061
QY 1341 CGCGTGGTTCCTCACTGCGCACATCGACTTCCACCTCGAGCGCGGGCTTCGCGATC 1395
Db 1062 GTCCCGCTCCATCTCTCCCGCGCTACATCCGCCCATGTCGCGCGGCACACGATC 1116

RESULT 10

US-09-954-456-700
; Sequence 700, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 700
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-700

Query Match 3.1%; Score 46.2; DB 10; Length 2838;
Best Local Similarity 47.7%; Pred. No. 0.023;
Matches 135; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 962 GCGTCGACAAAGCGCTCAACCTCGCGTTAACTTCAACGGCACCACCACTTCTTCAACA 1021
Db 209 GCGGCGGAGAGACGCGGACCGCGGACTGCTGCTCGCCCCAGCTGCGGGGCGGCCGCG 268
QY 1022 ACGCGACTTTACGCGCGGACCGCTCCCGGTACTCTCTCCAGATTCTGAGCGTGCAG 1081
Db 269 CCGAGCCCCCGGCGGAGCGCGCTCCCGGGCGCTGCGCGCGCGCGCGCGCGGAGC 328
QY 1082 CGGCACAAAGACCTGCTCCTGCAAGGCTGTCTACCGCTCCCGGCCACTCGACCATCG 1141
Db 329 GCGCCATGACGCGCTGCGCGCGCGCTTGCCTGCGCGCTGGCGCGAGCCACCCCGC 388
QY 1142 AGATCAGCTGCGCGGACCGCTTGGCCCGGGTGCACCGCTCCACCTTCCACCTCGAG 1201
Db 389 AGGGCCCGCGGCGCGGACCTTGGCAACCCGAGGCTGCGCACCCCGCGCGCTCTACA 448
QY 1202 GTCACGCTTCGCGGTCGTTTCGAGCGCGGGGAGCACACCGTA 1244
Db 449 GTCCACGCGCGCGTGGAGCGCGGAGACGAGAACAGTA 491

RESULT 11

US-09-954-456-966
; Sequence 966, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76

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; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 956
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-966
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Query Match          3.18; Score 46.2; DB 10; Length 2838;
Best Local Similarity 47.7%; Pred. No. 0.023;
Matches 135; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 962 CGGTGACAGCGCTCAACCTCGGTTTAACTTCAACGGCAGCAACTTCTTTCATCAACA 1021
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 GCGGCGGAGAGCGGACCGCGCACTGCTCTGCCCGAGCTGGCGGGCGCCCGCG 268

Qy 1022 ACGGACTTTCACGCGCGCGGACCGTCCCGGTACTCTCCAGATTCTGAGCGGTGGCAGA 1081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 CCGAGCCCCCGCGCGAGCGCGTCCCGCGCGCTGCCCGCGCGCGCGCGCGGAGC 328

Qy 1082 CCGCACAGACCTGCTCCCTCCAGGCTGTCTACCGCGCTCCCGCGCGCTGCCCGCGCG 1141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 GCGCCCATGACAGCGCTGCCCGCGCGCTTGGCTGGCGGCTGGCGCGGACCGCCCGC 388

Qy 1142 AGATCAGCTCCCGCGCGCGCGCGTGGCCCGCGGTGGCCAGCCACCCCTTCACCTGCACG 1201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 AGGCGCGCGCGCGCGCGCTTGGCAACCCGAGGCTGCGCAGCCCGCGCGCTCTACA 448

Qy 1202 GTCAGCGCTTCGCGGTGTTCCGAGCGCGGGGAGCAGCACGTA 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 GTCCGACGCGCGCGTGGCGCGGAGCAGAGAACGACAAGTA 491
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RESULT 12
US-09-954-456-1143
; Sequence 1143, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
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; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1143
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1143

Query Match          3.18; Score 46.2; DB 10; Length 2838;
Best Local Similarity 47.7%; Pred. No. 0.023;
Matches 135; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 962 CGGTGACAGCGCTCAACCTCGGTTTAACTTCAACGGCAGCAACTTCTTTCATCAACA 1021
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Db 209 GCGGCGGAGAGCGGACCGCGCACTGCTCTGCCCGAGCTGGCGGGCGCCCGCG 268

Qy 1022 ACGGACTTTCACGCGCGCGGACCGTCCCGGTACTCTCCAGATTCTGAGCGGTGGCAGA 1081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 CCGAGCCCCCGCGCGAGCGCGTCCCGCGCGCTGCCCGCGCGCGCGCGCGGAGC 328

Qy 1082 CCGCACAGACCTGCTCCCTCCAGGCTGTCTACCGCGCTCCCGCGCGCTGCCCGCGCG 1141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 GCGCCCATGACAGCGCTGCCCGCGCGCTTGGCTGGCGGCTGGCGCGGACCGCCCGC 388

Qy 1142 AGATCAGCTCCCGCGCGCGCGTGGCCCGCGGTGGCCAGCCACCCCTTCACCTGCACG 1201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 AGGCGCGCGCGCGCGCTTGGCAACCCGAGGCTGCGCAGCCCGCGCGCTCTACA 448

Qy 1202 GTCAGCGCTTCGCGGTGTTCCGAGCGCGGGGAGCAGCACGTA 1244
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Db 449 GTCCGACGCGCGCGTGGCGCGGAGCAGAGAACGACAAGTA 491
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RESULT 13
US-09-815-242-4093
; Sequence 4093, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
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QY	936	TGTTGCTTGGCAGCCCGACACCCGGGGGGTGCACAAGGGGCTCAACCTCGCGCTTTAACTT	995
Db	1246	GCTCAGGGCCATGGGGCTGCTGGCGCTGCTGGATGAGGAGCAGCTCTGGGGCGAAAGTGTCTC	1305
QY	996	CAACGGCACCAACTTCTTCATCAACAAGCGACTTTACGGCGCGAGCGTCCCGGTACT	1055
Db	1306	GCAGCGCGGGACCGTCTCTGGACAGCAACACACGCTGGGCGTCTTGGCCAGGCGCCACGG	1365
QY	1056	CCTCCAGATTCTGAGGGTGGCGCAGACCGCAACAAGACCTGCTCCCTGCAAGGCTCTGTCTA	1115
Db	1366	CCCCCAGGGCCCGCGCGACGCTGGCGCGCGCGGTGCTGATCTACGGGAGCGACGACAC	1425
QY	1116	CCCGCTCCCGGCCCACTCCACCATCGAGATCAGCTGCCCCGCGACGCGCTTGGCCCCGGG	1175
Db	1426	CCGCGCCACCCCAACCGCAGGTCGCGGTGACCTTGGGGTGGCGGGGTGCCCGCGG	1485
QY	1176	TGCACCGCACCCCTTCCACCTGCACGGTCACGCCCTTCGCGGTCTGTCGACGCGCGG	1232
Db	1486	CCCGGGCTGTGTCTACGTACAGCGCTACCTGGACAAACGGGCTCTGCAGCCCCGACGG	1542

Search completed: December 14, 2002, 06:53:26
Job time : 332 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:07:26 ; Search time 262 seconds
(without alignments)
12893.120 Million cell updates/sec

Title: US-09-786-960-1

Perfect score: 1500

Sequence: 1 gccatcgccgctggcgag.....tgagcgaggtaccacgtga 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1500	100.0	1500	21	Trametes versicolor
2	1500	100.0	1500	24	Trametes versicolor
3	917.8	61.2	1563	24	Trametes versicolor
4	892.2	59.5	1497	11	Phenol oxidase (PO)
5	892.2	59.5	1497	11	Sequence encoding
6	890.6	59.4	1497	11	Sequence encoding
7	874.8	58.3	1572	20	T. versicolor lacc
8	871.6	58.1	1572	20	T. versicolor lacc
9	771.3	51.5	2880	17	Laccase-LCC2 gene.

10	755.4	50.4	7986	20	AAZ23937	T. versicolor lacc
11	519	34.6	1722	21	AAA57402	cDNA sequence enco
12	519	34.6	1722	21	AAA57439	cDNA sequence enco
13	515.4	34.4	1822	19	AAV28293	Schizophyllum comm
14	509.4	34.0	1801	24	ABK50850	DNA encoding Lenti
15	472.6	31.5	1170	18	AAAT67137	Coprinus cinereus
16	452.8	30.2	2418	17	AAAT15598	Laccase-LCC1 gene.
17	448.4	29.9	5762	20	AAZ23938	T. versicolor lacc
18	439.6	29.3	1161	18	AAAT67138	Coprinus cinereus
19	413.8	27.6	1874	24	ABK50851	DNA encoding Lenti
20	393.6	26.2	2289	24	ABK50852	DNA encoding Lenti
21	377.6	25.2	1176	18	AAAT67136	Coprinus cinereus
22	342	22.8	1835	24	ABK50853	DNA encoding Lenti
23	310.6	20.7	2049	11	AAQ03366	Phenol oxidase (PO)
24	310.6	20.7	2049	11	AAQ03573	Phenol oxidase gen
25	257.8	17.2	3284	20	AAQ02677	T. versicolor lacc
26	245.6	16.4	1588	21	AAZ24235	R. solani laccase
27	245.6	16.4	1672	16	AAQ86526	Laccase gene RSLac
28	244	16.3	1588	18	AAAT63317	Rhizoctonia solani
29	223	14.9	3566	18	AAAT69338	Coprinus cinereus
30	212.4	14.2	2940	18	AAAT69337	Coprinus cinereus
31	209.8	14.0	2122	13	AAQ20956	Laccase gene. Phl
32	186	12.4	3327	18	AAQ69336	Coprinus cinereus
33	182.8	12.2	2860	17	AAAT15601	Laccase-LCC4 gene.
34	156.2	10.4	2925	17	AAAT15602	Laccase-LCC5 gene.
35	123	8.2	3116	24	ABK15406	DNA encoding Melan
36	112.6	7.5	2249	18	AAAT74283	Cellulose binding
37	112.6	7.5	2279	18	AAAT74281	Cellulose binding
38	112.6	7.5	2300	18	AAAT74282	Cellulose binding
39	109.4	7.3	2476	18	AAAT67234	Scytalidium thermo
40	106.6	7.1	3102	17	AAAT15600	Laccase-LCC3 gene.
41	106.2	7.1	3192	18	AAAT63318	Myceliophthora the
42	105.2	7.0	3187	17	AAAT10922	Laccase gene. Myc
43	105.2	7.0	3192	18	AAAT72106	Myceliophthora the
44	105.2	7.0	3192	21	AAZ24236	M. thermophila lac
45	104.8	7.0	2604	23	ABL13475	Drosophila melanog

ALIGNMENTS

```

RESULT 1
AAA09191
ID AAA09191 standard; DNA; 1500 BP.
XX
AC AAA09191;
XX
DT 10-AUG-2000 (first entry)
XX
DE Trametes versicolor laccase coding sequence.
XX
KW Laccase; transgenic plant; large scale production; paper; pulp;
KW lignin; degradation; biosynthesis; ds.
XX
OS Trametes versicolor.
XX
PN WO200020615-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23256.
XX
PR 05-OCT-1998; 98US-0103031.
XX
(P-PROD-) PRODIGENE INC.
XX
Hood E, Howard J, Jilka J;
XX
WPI; 2000-303793/26.
XX
P-PSDB; AA92248.
XX
Industrial scale laccase production in recombinant corn and maize
plants to produce enzymes for use in the paper industry

```

XX PS Claim 9; Page 17-19; 34pp; English.

XX CC The Trametes versicolor laccase gene can be used to create transgenic

CC plants which produce laccase at levels of about 0.01% or higher of the

CC total soluble protein of the plant. The transgenic plants may be used

CC for the large scale production of laccase enzymes. Laccase is mainly

CC used in the paper and pulp industry for breaking down lignin.

CC Conversely, laccase is also involved in lignin biosynthesis and the

CC formation of lignin polymers. It is therefore useful as a biological

CC adhesive for gluing wood (e.g. in the production of plywood, oriented

CC strand board, particle board and medium density fiberboard). Laccase

CC may also be used for catalyzing the oxidation of compounds such as

CC o,p-diphenols, aminophenols, polyamines and inorganic ions. It is

CC also used as a marker enzyme in enzyme immunoassays, for the oxidation

CC of steroids and the synthesis of vinblastine (a cytostatic compound

CC used in treating malignant diseases).

XX SQ Sequence 1500 BP; 275 A; 551 C; 402 G; 272 T; 0 other;

Query Match 100.0%; Score 1500; DB 21; Length 1500;

Best Local Similarity 100.0%; Pred. No. 3.2e-284;

Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCATCGGGCGGTCGAGCGCTCGTCTCGGAGCGCCCGCTCGCGAGCGGCTTC 60

DB 1 GCCATCGGGCGGTCGAGCGCTCGTCTCGGAGCGCCCGCTCGCGAGCGGCTTC 60

QY 61 CTTTCGGGATGCATCGTGGTCAAGCGGCTGGTCCCTTCCCGGCTCATCACCGGGAAGAAG 120

DB 61 CTTTCGGGATGCATCGTGGTCAAGCGGCTGGTCCCTTCCCGGCTCATCACCGGGAAGAAG 120

QY 121 GGAGACCGGTCGAGCTCAAGTGTGACACCTTGACACCTTGACACCGGAGCTCAAGTCC 180

DB 121 GGAGACCGGTCGAGCTCAAGTGTGACACCTTGACACCGGAGCTCAAGTCC 180

QY 181 ACTAGTATCCACTGCGCGGCTTCTTCCAGGAGGACCACTTGGGAGCGGACCGCCGCG 240

DB 181 ACTAGTATCCACTGCGCGGCTTCTTCCAGGAGGACCACTTGGGAGCGGACCGCCGCG 240

QY 241 TTCGTCAACCAAGTGCCTTATGCTTCCGGGATTCATTTCTGTAGGACTTCCATGTGCC 300

DB 241 TTCGTCAACCAAGTGCCTTATGCTTCCGGGATTCATTTCTGTAGGACTTCCATGTGCC 300

QY 301 GACGAGGAGGAAGCTTCTGTGACACAGTATCTGTAGCAATATCTGTGACGGGCTG 360

DB 301 GACGAGGAGGAAGCTTCTGTGACACAGTATCTGTAGCAATATCTGTGACGGGCTG 360

QY 361 CGAGGACCGTTCGTGTGTGACACCGGCTTCCAGGATCCGACGCGGCTAGCATGTTGAC 420

DB 361 CGAGGACCGTTCGTGTGTGACACCGGCTTCCAGGATCCGACGCGGCTAGCATGTTGAC 420

QY 421 AACGAGACCGGTATCATCGTTGACGCTTGTACGCTGCTGACGCGGCTCGGCTCGCTCC 480

DB 421 AACGAGACCGGTATCATCGTTGACGCTTGTACGCTGCTGACGCGGCTCGGCTCGCTCC 480

QY 481 AGGTTCCCACTCGGCGGAGCGGCTTGTGATCAATGCTTGTGGCGGTTCGCGCTCCACT 540

DB 481 AGGTTCCCACTCGGCGGAGCGGCTTGTGATCAATGCTTGTGGCGGTTCGCGCTCCACT 540

QY 541 CCGACCGCGGCTTGTGTGTGATCAAGCTTCCAGGACGCGGAAAGCGCTACCGCTTCGCTC 600

DB 541 CCGACCGCGGCTTGTGTGTGATCAAGCTTCCAGGACGCGGAAAGCGCTACCGCTTCGCTC 600

QY 601 GTTTCGATCTGTCGACCGGCTTGTGATCAAGCTTCCAGGACGCGGAAAGCTTGTACCGCTC 660

DB 601 GTTTCGATCTGTCGACCGGCTTGTGATCAAGCTTCCAGGACGCGGAAAGCTTGTACCGCTC 660

QY 661 ATCGAGGTCGAGGATATCAAGCGGCTTGTGATCAAGCTTCCAGGACGCGGAAAGCTTGTAC 720

DB 661 ATCGAGGTCGAGGATATCAAGCGGCTTGTGATCAAGCTTCCAGGACGCGGAAAGCTTGTAC 720

QY 721 GCGCAGCGCTACTCTCTTTGTTGATGCAACCAAGCTTCGCAACTACTTGGGTCCGC 780

DB 721 GCGCAGCGCTACTCTCTTTGTTGATGCAACCAAGCTTCGCAACTACTTGGGTCCGC 780

QY 781 GCGAACCCGAATTCGGAACGGTTGGTTGCGCGGGGGATCAACTCCGCCATCTCTGCGC 840

DB 781 GCGAACCCGAATTCGGAACGGTTGGTTGCGCGGGGGATCAACTCCGCCATCTCTGCGC 840

QY 841 TACCAAGGCGACCTGCGCGGAGCCCACTTACGACCCAGACGACGTCGGTGTATCCCGCTT 900

DB 841 TACCAAGGCGACCTGCGCGGAGCCCACTTACGACCCAGACGACGTCGGTGTATCCCGCTT 900

QY 901 ATCGAGACGAATTCGACCCCTCGCTCGCATGCTTGTGCTGCGAGCCGACACCCGGG 960

DB 901 ATCGAGACGAATTCGACCCCTCGCTCGCATGCTTGTGCTGCGAGCCGACACCCGGG 960

QY 961 GCGCTGACAAAGCGCTCAACCTCGGCTTAACTTCAACGGGACCAACTTCTTTCATCAAC 1020

DB 961 GCGCTGACAAAGCGCTCAACCTCGGCTTAACTTCAACGGGACCAACTTCTTTCATCAAC 1020

QY 1021 AACGCGACTTTCACGCGCGGAGCCGCTCCCGGTACTCTCCAGATTCTGAGCGGTGGCGAG 1080

DB 1021 AACGCGACTTTCACGCGCGGAGCCGCTCCCGGTACTCTCCAGATTCTGAGCGGTGGCGAG 1080

QY 1081 ACCGCAAGACCTGCTTCCCTGCGAGCTTGTCTACCCGCTCCCGGCGGCTCCACCATC 1140

DB 1081 ACCGCAAGACCTGCTTCCCTGCGAGCTTGTCTACCCGCTCCCGGCGGCTCCACCATC 1140

QY 1141 GAGATCAGCTGCGCGGAGCGCTTGGCCCGGCTGCGAGCGCGGGAGCACCAGTATAACTACAAGACCCG 1260

DB 1141 GAGATCAGCTGCGCGGAGCGCTTGGCCCGGCTGCGAGCGCGGGAGCACCAGTATAACTACAAGACCCG 1260

QY 1261 ATCTTCGCGGAGCTGTGAGACGGGACGCGCGCGGCGGCGGAGCACCAGTATAACTACAAGACCCG 1320

DB 1261 ATCTTCGCGGAGCTGTGAGACGGGACGCGCGCGGCGGCGGAGCACCAGTATAACTACAAGACCCG 1320

QY 1321 TTCCAGACGGAAACCCCGGCGCTGTTCTTCCACTGCCACATCGACTTCCACCTCGAC 1380

DB 1321 TTCCAGACGGAAACCCCGGCGCTGTTCTTCCACTGCCACATCGACTTCCACCTCGAC 1380

QY 1381 GCGGGCTTCGGGATCGTTCGAGAGGACGCTTCCGAGACGCTTCCGAGGCGGAGGCGGAAACCCGTT 1440

DB 1381 GCGGGCTTCGGGATCGTTCGAGAGGACGCTTCCGAGACGCTTCCGAGGCGGAGGCGGAAACCCGTT 1440

QY 1441 CCGAAGGCTGCTGCGGACCTGTCGCCGATCTACGACGGGCTGAGCGAGGCTTAACAGTGA 1500

DB 1441 CCGAAGGCTGCTGCGGACCTGTCGCCGATCTACGACGGGCTGAGCGAGGCTTAACAGTGA 1500

RESULT 2

ABA92910

ID ABA92910 standard; cdna; 1500 BP.

XX ABA92910;

AC ABA92910;

DT 09-APR-2002 (first entry)

XX Trametes versicolor laccase I gene.

XX Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;

KW copper; metal cofactor; gene; plant; ds.

XX Trametes versicolor.

OS

XX Key Location/Qualifiers

FT CDS 1..1500

FT /*tag= a

FT /product= "laccase I"

FT /note= "no start codon given"


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RESULT 3
ID ABL60268 standard; cDNA; 1563 BP.
XX
XX ABL60268;
XX
XX 23-AUG-2002 (first entry)
XX
XX Trametes versicolor Laccase III encoding cDNA SEQ ID NO 25.
DE
XX Fungi; Thal; copper-dependent secreted protein; copper; laccase;
KW Trametes ATX1 homologue; copper transporting ATPase; gene; ss.
XX
XX Trametes versicolor.
XX
XX Key Location/Qualifiers
FH 1..1563
FT CDS
FT /*tag= a
FT /product= "Laccase III"
XX
XX DE10046932-A1.
XX
XX 16-MAY-2002.
XX
XX 21-SEP-2000; 2000DE-1046932.
XX
XX 21-SEP-2000; 2000DE-1046932.
XX
XX (CONE ) CONSORTIUM ELEKTROCHEM IND GMBH.
XX
XX Marbach-Ringhandt K, Pfaller R, Uldschmid A;
XX
XX WPI; 2002-445163/48.
XX
XX P-PSDB; ABB77510.
XX
XX Expression system for increased production of copper-dependent enzymes,
XX particularly laccase, includes the gene for a copper homeostasis
XX protein
XX
XX Example 9; Page 46-48; 58pp; German.
XX
XX The invention relates to an expression system (A) that provides increased
XX expression of copper-dependent secreted proteins (I) in eukaryotic cells
XX comprises a gene (II) that encodes (I) and at least one cooper
XX homeostasis gene (III). (A) is used to express enzymes, especially
XX laccase, that require copper as co-factor. (III) transports copper to the
XX secretory pathway so its overexpression leads to increased yields of (I).
XX The present sequence is that of the Trametes versicolor Laccase III
XX encoding polynucleotide of the invention.
XX
XX Sequence 1563 BP; 271 A; 603 C; 384 G; 305 T; 0 other;
XX
XX Query Match 61.2%; Score 917.8; DB 24; Length 1563;
XX Best Local Similarity 75.8%; Pred. No. 1.9e-170;
XX Matches 1135; Conservative 0; Mismatches 362; Indels 0; Gaps 0;
XX
XX 4 ATCGGGCGGCTGGAGCGCTCGTCGCGAAGCGCCCGCTCTCGCCGCGAGCGTTCCTT 63
XX
XX 67 ATCGGTCTCTGTCGCGACCTCACCATCACCAGCGAGCGGTGAGCCCGCGGTTTCT 126
XX
XX 64 CGGGATGCCATCGTGGTCAACGGCGTGGTTCCTCCCGCTCATCCGCGGAAGAAGGA 123
XX
XX 127 CGCCAGGCGTCTGTCGTAACGCGCGCACCCCTGCGCTCTCATCACCAGTAACATGGG 186
XX
XX 124 GACCGTTCCAGCTAACGTCGTGACACCTTGACACCAACCAAGCATGCTCAAGTCCACT 183
XX
XX 187 GATCGCTCCAGTCAATGTCATGACACACCTTCAGAACACACACGATGCTGAAGAGCAC 246
XX
XX 184 AGTATCCACTGCGAGGCTTCTTCAGGCGAGGACCACTGGGCGAGCGGCCCGGTTTC 243
XX
XX 247 AGTATTCAGTGCAGGTTTCTTCAGAGGACCACTGGGCGAGCGGTCCCGCTTC 306
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Db 1387 CGACCCGACAAACCCCGCGTGGTTCCTCCACTGCCACATCGACTTCACCTCGAGGCC 1446
QY 1384 GCGTTCGCGATCGTGTTCGACAGGACGTTGCGGACGTGAAGCGCGGAACCGGTTCCG 1443
Db 1447 GCGTTCGCGCGTGTGTTCGCGGAGGACATCCCGGACGTGCGGCGAACCCCGTCCCG 1506
QY 1444 AAGGCGTGTGCGACCTGTGCGCGATCTACGACGGGCTGAGCGAGGCTAACCACTGA 1500
Db 1507 CAGGCGTGTGCGACCTGTGCGCGACTAGGACGGCTCGACCCGACGACCAAGTAA 1563

RESULT 4

AAQ03367
ID AAQ03367 standard; DNA; 1497 BP.

XX AAQ03367;

XX 18-AUG-1990 (first entry)

XX Phenol oxidase (PO) gene.

DE Phenol oxidase (PO) gene.

KW Phenol oxidase (PO) gene; enzyme.

XX JP02005877-A.

XX 10-JAN-1990.

XX 16-JUN-1988; 88JP-0149103.

XX 16-JUN-1988; 88JP-0149103.

XX (OJIP) OJI PAPER KK.

PA WPI: 1990-053914/08.

DR P-PSDB; AAR05279.

XX Phenol oxidase gene - used for biological pulping, etc.

XX Page 812-813; Fig 2; 14pp; Japanese.

XX It can be used to transform various organisms to produce new organisms
CC that produce enormous amts. of PO. The PO produced is very pure and is
CC useful as a biochemical or diagnostic reagent. Also new are a phenol
CC oxidase gene capable of hybridizing to it, and recombinant DNA
CC consisting of this gene or AAN93367 ligated with vector DNA.

XX Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 59.5%; Score 892.2; DB 11; Length 1497;
Best Local Similarity 74.7%; Pred. No. 1.9e-165;
Matches 1119; Conservative 0; Mismatches 378; Indels 0; Gaps 0;

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Db 1 GCATCGGCGCGCGCTGACCTCACCCTCCTCCATGCGGAGTACGCCCGGATGGGTTTC 60

QY 61 CTTTCGGGATGCCATCGTGTGTAACGCGGTGTCCTTCCCGCTCATCACCGGGAAGAAG 120

Db 61 GCTGTCAGGCTGTGTTGTCAACAATGTTACCCCGGAGCCCTGCTGCGGGCAACAAG 120

QY 121 GGAGACCGGCTCCAGCTCAACCTGCTCGACACCTTGACCAACACAGCATGCTCAAGTCC 180

Db 121 GGTGACCGGCTTCCAACTCAATGTATCGACAACCTTCACGAACCACTATGCTGAAGAGC 180

QY 181 ACTAGTATCCACTGGCACCGCTTCTTCCAGGAGGAGGACCAACTGGGACAGGACCGCGG 240

Db 181 ACGAGTATCCACTGGCATGCTTCTTCCAGAGGAGGAGCAAACTGGGCTGATGTTCCCGG 240

QY 241 TTCGTCACCAAGTGCCTTATTCGTCGGGCAATTCATTTCTAGACATTCATGTCGCC 300

Db 241 TTTGTGAACCAAGTGCCCTATTTCCTCTGGGCACTGTTCTCTACGATTTCCAGGTTCT 300

QY 301 GACGAGCGAGGAACGTTCTGGTACCACAGTCACTCTGTCTACGCAATACTGTGACGGGCTG 360
Db 301 GACGAGCGCGGTACCTTCTGGTACCACAGCCACTTGTCCACTAGTACTGTGACGGGCTG 360
QY 361 CGAGGACCGTTCGTGCTGTACGACCCCAAGGATCCGACGCCAGCGCTACGATGTTGAC 420
Db 361 CGGGGTCCTTTCGTGCTGTACGATCCCAATGACCCCGACGCGAGTTGTATGACGTCGAC 420
QY 421 AACGAGSACAGGTCATCAGTTGACCGACTGTGTACACACACGCTGCCGGCTCGGTCC 480
Db 421 AATGACGACAGCGGTGATCAACCTCGCGGATTTGGTACACACTCCCGAAGCTCGGCC 480
QY 481 AGGTTCCCTACTCGGCGCGGACGCCAGCTCATCAATGGTCTTGGCGGGTCCGGCTCCACT 540
Db 481 GCGTTCCCTACTCGGTCGGGATGCTACCTTATCAACGGGCTCGGGCTTCCCCAGCACC 540
QY 541 CCCACCGCGCGCTTCTGTGTATCAAGCTCCAGCAGCGGAAGCGCTACCGCTTCCGTCTC 600
Db 541 ACGGCGCGGACCTCGCAGTCACTCAACGTCACGAAGGCAAAAGCTACCGTTTCCGCTG 600
QY 601 GTTTCGATCTCGTGCAGCCGAACTACAGTTTCAGCATCGACGGGCACATCTGACCGTC 660
Db 601 GTCTCCTCTGTGTGATGACCCCAACACAGCTTCAGCATCGATGGTCATGACTTGSAGATC 660
QY 661 ATCGAGTCCGAGGTATCAACAGCCAGCCTCTCTTGTGTGACTCTATCCAGATCTTCGCC 720
Db 661 ATCGAGTGGACTTCCATCAACTCGCAACCTCTGGTGGTGTGACTCCATCCAGATTTCCGT 720
QY 721 GCGAGCGCTACTCTCTTGTGTGATGGAACCAACGCTCGGCAACTACTTGGTCCGCG 780
Db 721 GCGAGCGTACTCTCTTGTGTGATGCGCACAGGATGTCGGTAACCTACTTGGATTCGC 780
QY 781 GCGAACCCGAACCTTCGGAACGTTGGTTCGCGGGGGGATCAACTCCGCCATCTCGCG 840
Db 781 GCCAACCCCAACTTCGGAACGTCGGATTTGCGGGTGGTATCAACTCGGCCATCTTCGCC 840
QY 841 TACCAAGSCGACACAGTCCGCGAGCCCACTTACGACCCAGACGACGTCGGTGTATCCGCTT 900
Db 841 TACGACGCGCGGACCCCGTTGAGCCCAACGACGACTAGCTACGCGCAAGACCCCTG 900
QY 901 ATCGAGACGAACCTTGACCCCGCTCGCTCGCATGCTGTGCTGGGAGCGGACACCGCGG 960
Db 901 AACGAGGTGCACTTGACCCCGCTCGCCACCATGGCTGTGCCCGGTTCCCGAGTCGCGGT 960
QY 961 GCGCTCGACAAGCGCTCAACCTTCGCGTTTAACTTCAAGCGGACCAACTTCTTCATCAAC 1020
Db 961 GGTGTGACACGCGTATCAACATGGCTTCAACTTCAATGGTACCAACTTCTTCATCAAC 1020
QY 1021 AAGCGACATTTTCAGCGCGCGGACCGCTCCCGGTACTCTCCAGATTTCTAGCGGTGGCAG 1080
Db 1021 GCGCGAGCTTTTGTGCCCCCAACCGTSCGCGTCTCTGCTCCAGATCATCAGCGCGCCAG 1080
QY 1081 ACGGCAACAGACTGCTCTCGAGGCTCTGTCTACCGCTCCCGCGCCACTCCACCATC 1140
Db 1081 AAGGCCAGGATCTCTCCCGTCTGCGAGGCTACTCCCTCCGTCGAACGCGGATATC 1140
QY 1141 GAGATCACGCTGCCCGGACCGCTTGGCCCCGGGTGTCACCGACACCCCTTCCACCTGCAC 1200
Db 1141 GAGATCTCTCTCTGCTACGCGCGCTGCTCGGGTGCCTTCCCGCTTCCACCTTGCAC 1200
QY 1201 GGTACGCTTCCGCGTCTGTCGACGCGGGGAGGACCACTATCACTACACGACCCG 1260
Db 1201 GGTACGCTTCCGCGTCTGTCGCTAGCGTGGCAGCACCCTTACAACTACGACAACCC 1260
QY 1261 ATCTTCCGCGAGCTCGTGAGCACGCGCGCGCGGGGACAACTGACGATCCCG 1320
Db 1261 ATCTTCCGCGAGCTCGTGAGCACGCGCTCGCGCGGTGACAACTGACCATCCCG 1320
QY 1321 TTCGAGACGGAACACCCCGGCGGTGTTCTTCCACTGCCACATCGACTTCCACCTCGAC 1380
Db 1321 TTCGAGACGGAACACCCCTTGGTCTTCCCTCCACTGCCACATCGACTTCCACCTTGA 1380
QY 1381 GCGGGCTTCGCGATCGTGTTCGAGAGGAGCTTGGGAGCTGGAAGCGCGGACCCGGTT 1440

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1381 GCCGGCTTTGCGGTGTTGCGGGAGGACATCCCGACGTGCGGTGCGGGAACCCCGTC 1440
1441 CCGAAGCGGTGGTGGGACCTGTGCCGATCTAGCAGGGCTGAGCGAGGCTAACCAG 1497
1441 CCTCAGCATGGTCTGATCTGTGTCGCCCATCTATGACGCACTCGATGTCACGACCA 1497

RESULT 5
AAQ03571
ID AAQ03571 standard; DNA; 1497 BP.
AC AAQ03571;
XX
XX 03-FEB-1991 (first entry)
XX
XX Sequence encoding phenol oxidase (PO).
XX
XX Paper pulping; ds.
XX
XX JP02027986-A.
XX
XX 30-JAN-1990.
XX
XX 15-JUL-1988; 88JP-0175236.
XX
XX 15-JUL-1988; 88JP-0175236.
XX
XX (OJIP ) OJI PAPER KK.
XX
XX WPI; 1990-323326/43.
XX
XX P-PSDB; AAR07068.
XX
XX New phenol oxidase gene - has DNA encoding specified sequence of
XX 499 aminoacid(s)
XX
XX Claim 4; Fig 2; 15pp; Japanese.
XX
XX PO is useful in biological paper pulping and bleaching.
XX
XX Sequence 1497 BP; 272 A; 535 C; 378 G; 312 T; 0 other;

Query Match 59.5%; Score 892.2; DB 11; Length 1497;
Best local Similarity 74.7%; Pred. No. 1.9e-165;
Matches 1119; Conservative 0; Mismatches 378; Indels 0; Gaps 0;

QY 1 GCCATCGGGCGGTGGGAGCGCTCGTGCAGAACGCCGCCGCTCGCGGACGGGCTC 60
DB 1 GCCATTGGGCCCCACCGCTGACCTCACCATCTCCAATGCCGAGGTACGCCCGGATGGGTT 60
QY 61 CTTCCGGATGCCATCGTGGTCAACGGGTGTGTCCTTCCCGCTCATCACCGGGAAGA 120
DB 61 GCTCGTCAGGCTGTGGTGTCAACAATGTATACCCGGGACCCCTCGTCGGGGCAACA 120
QY 121 GGAGACCGTTCCAGTCTCAAGTCTCGACACCTGTGACACCTTGACCAACACAGATGCTCAAGTCC 180
DB 121 GGTGACCGCTTCCAACTCAATGTATGACAACTCATGCAACCTCAGAACCACTATGCTGAAGAGC 180
QY 181 ACTAGTATCCACTGCGAGGCTTCTCCAGCAGGACCACTCGGCGAGAGGACCGCG 240
DB 181 ACGAGTATCCACTGCGATGGCTTCTCCAGAGGGGACAACTGGGCTGATGGTCCCGCG 240
QY 241 TTCGTCAACAGTGCCTATTGCTTCGGGCATTCATTCTGTACGACTTCCATGTGCC 300
DB 241 TTTGTGAACAGTGCCTATTTCCTCTGGGCACCTGTTCTCTACGATTTCAGGTTTCT 300
QY 301 GACCAGGAGGAAGTCTGTGTACACAGTATCTGTCTAGCAGTACTGTGACGGGCTG 360
DB 301 GACCAGGCGGTACTCTGTGTACACAGGCACTGTGTCACCTAGTACTGTGACGGGCTG 360
QY 361 CGAGACCGTTCGCTGTGTAGACCCCAAGATCCGACGCGCCACCGCTAGGATGTGAC 420
DB 361 CCGGCTCTTTCGCTGTGTAGTATCCCAATGACCCGACGGAGTTGTGTATGACGTGAC 420
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QY 421 AACGAGAGCACGGTTCATCAGCTTGACCGACTGTTACACACCGCTGCCCGGCTCGGTCCC 480
DB 421 AATGACGACACCGTGTATCAACCTCGCGGATTGGTACCACACTGCGCGAAGCTCGGCCCC 480
QY 481 AGGTTCCCACTCGCGCGGAGCGACGCTCATCAATGGTCTTGGCGGCTGCGGCTCCACT 540
DB 481 GCGTTCACACTGGGTGCGGATGTACCTTTATCAACGGGCTCGGGCTTCCCGAGCACC 540
QY 541 CCCACCGCGCGCTTGCTGTGATCAACGTCAGCACGAAAGCGCTACCGTTCGCTC 600
DB 541 ACGCGCGGACCTCGCAGTCATCAACGTCAGAAAGGCAACCGCTACCGTTCGCGCTG 600
QY 601 GTTTCGATCTCGTGACCGGAACTACACGTTTCAGCATCGACGGGCAACAATTCACCGTC 660
DB 601 GTCTCCTGTGTGACCCCAACACACAGTTCAGCATCGATGTGTCATGACTTCAGCATC 660
QY 661 ATCGAGTGCAGGTATCAACAGCGGCTCTCTTGTGACTATATCCAGATTTGCGC 720
DB 661 ATCGAGTGGACTCCATCAACTCGCAACCTCTGTTGGTTGACTCCATCCAGATTTGCGT 720
QY 721 GCGCAGCGTACTCTCTTGTGTAATCGAACAACGTCGCGCAACTACTTGGTCCGC 780
DB 721 GCGCAGCGTACTCTCTTGTGTAATCGAACAACGTCGCGCAACTACTTGGTCCGC 780
QY 781 GCGAACCCGAACCTTCGGAACGTTGGTTCGCGGGGGGATCAACTCCGCCATCCTCGC 840
DB 781 GCCAACCCGAACCTTCGGAACGTTGGTTCGCGGGGGGATCAACTCCGCCATCCTCGC 840
QY 841 TACCAAGGCGCACCAGTCCGCGAGCCCACTAGCAGCCAGAGGAGTGGTGTATCCCGCTT 900
DB 841 TAGCAGCGCGCAGCACCAGTTCGCGGCGGCGGCTGAGCCACCACTCAGACTCGCGCAAC 900
QY 901 ATCGAGAGCAACTTCACCCCTCGCTCGCATGCTGTGCTGGCAGCCCGCACCGCGG 960
DB 901 AACGAGTGCAGTTCGACCGCGCTCGCCACCATGCTGTGCCGCTTCCCGAGTCCGCGGT 960
QY 961 GGGTCGACAAAGCGCTCAACCTCGCGTTTAACTTCAACGCGACCAACTTCTTCATCAAC 1020
DB 961 GGTGTTGACAGCGCTATCAACATGGCTTCAACTCAATGTATCAACTTCTTCATCAAC 1020
QY 1021 AACCGGACTTCACGCGCGCGACCGTCCCGTACTCTCTCCAGATCTCGAGGCTGCGCAG 1080
DB 1021 GGCCGAGCTTTGTGCGCCCCACCGTCCGCTCTGCTCCAGATCATCAGCGGCGCCAG 1080
QY 1081 ACCGCAAGACCTGCTCCCTGCGAGGCTGTCTACCGCTCCCGCGCCACTCCACCATC 1140
DB 1081 AACGCCAGGATCTCTCCCTGCTGGCAGGCTCTACTCCCTCCGCTCAACGCGGATATC 1140
QY 1141 GAGATCAGCTGCGCGGACCGCTTGGCCCCGGGTGCACCGCACCCCTTCCACTCGCAC 1200
DB 1141 GAGATCTGTTCCCTGCTACGGCGGTGCTCCGGGTGCCCCCTCACCCCTTCCACTTGAC 1200
QY 1201 GGTCAAGCTTCGCGGCTGCTGCGAGCGCGGGGAGCACCAGTATACTACAAGACCCG 1260
DB 1201 GGTCAAGCTTCGCGGCTGCTGCGAGCGCGGGGAGCACCAGTATACTACAAGACCCG 1260
QY 1261 ATCTTCGCGAGCTGCTGAGCAGCGGACGCGCGCGCGGCGGACAACTCAGCATCGCG 1320
DB 1261 ATCTTCGCGAGCTGCTGAGCAGCGGAGCGCTGCGGCGGCTGACAGCTCACCCTCGC 1320
QY 1321 TTCAGAGCGGAACACCGCGGCGCTGCTCTCACTGCCACATCGAGTTCACCTCGAC 1380
DB 1321 TTCGCAACGGAACACCGCGGCGCTGCTCTCACTGCCACATCGAGTTCACCTCGAG 1380
QY 1381 GCGGGCTTCGCGATGCTGTCGAGAGGAGCTTGGGAGCTGAAGGCGGCGCAACCGGTT 1440
DB 1381 GCGGGCTTCGCGATGCTGTCGAGAGGAGCTTGGGAGCTGAAGGCGGCGCAACCGGTT 1440
QY 1441 CCGAAGCGGTGCGGACCTGTGCGCGATCTACGACGGGCTGAGCGAGGCTTAACAG 1497
DB 1441 CCTCAGGATGCTGTGTCGCGGCTATGACGCACTCGATGTCAACAGCACCAG 1497
```

RESULT 6
AAQ03572
ID AAQ03572 standard; DNA; 1497 BP.
XX
AC AAQ03572;
XX
DT 03-FEB-1991 (first entry)
XX
DE Sequence encoding phenol oxidase (PO).
XX
KW Paper pulping; ds.
XX
PN JP02027986-A.
XX
PD 30-JAN-1990.
XX
PF 15-JUL-1988; 88JP-0175236.
XX
PR 15-JUL-1988; 88JP-0175236.
XX
PA (OJIP) OJI PAPER KK.
XX
WPI: 1990-323326/43.
DR P-PSDB; AAR07069.
XX
New phenol oxidase gene - has DNA encoding specified sequence of
PT 499 aminoacid(s)
XX
PS Claim 5; Fig 3; 15pp; Japanese.
XX
CC PO is useful in biological paper pulping and bleaching.
XX
SQ Sequence 1497 BP; 272 A; 536 C; 377 G; 312 T; 0 other;
Query Match 59.4%; Score 890.6; DB 11; Length 1497;
Best Local Similarity 74.7%; Pred. No. 3.9e-165;
Matches 1118; Conservative 0; Mismatches 379; Indels 0; Gaps 0;
QY 1 GGCATCGGCGCGTGGCGAGCCTGCTGTCGGGAAGCCCGCTCGCCCGACGGCTTC 60
Db 1 GGCATGCGCGCGCGCGCTGAGCTCCACATCTCCATGCGCGAGGTGAGCCCGATGGGTTTC 60
QY 61 CTTCGGGATGCCATGCTGTGTAACGGGTGGTCCCTTCCCGCTCATCACCGGGAAGAAG 120
Db 61 GCTGCTGAGGCTGTGGTTGTCAACAATGTTACCCCGGAGCCCTCTGTCGGGGACACAG 120
QY 121 GGAGACCGGTTCCAGTCAACGTCGTCGACACCTTGACCAACACAGCATGCTCAAGTCC 180
Db 121 GGTGACCGGTTCCAACTCAATGTCATCGACAACTTACGAAACACACTATGCTGAAGAGC 180
QY 181 ACTAGTATCCATGCGCAGCGCTTCTCCAGGAGGACCACTGGGCAGACGGACCCGCG 240
Db 181 ACGAGTATCCATGGCATGGCTTCTTCCAGAGAGGGAGACAACTGGGCTGATGTCGCCGG 240
QY 241 TTTCGCAACAGTGCCTTATTCCTCGGGCATTCATTTCTGTACGACTTCCATGTGCC 300
Db 241 TTGTGTAACAGTGCCTTATTCCTCTGGGCACTGTTCTCTACGATTCAGGTTCTCT 300
QY 301 GACAGGCGAGGAAGGTTCTGGTACCACTGTCATGTCGTACGCAATACGTGACGGGCTG 360
Db 301 GACCAAGGCGGTACCTTCTGGTACCACTGTCATGTCGCACTGTCAGTGTGACGGGCTG 360
QY 361 CGAGGACCGTCTGCTGTACGACCCCAAGGATCGCAGCGCGCGCTACCATGTTGAC 420
Db 361 CGGGGTCTTTCTGCTGTACGATCCCAATGACCCGCGAGGTTTGTATGACGTCGAC 420
QY 421 AACGAGACAGGTCATACGTTGACCGCATGTTACCAACCGCTGCCCGGCTCGGTC 480
Db 421 AATGACGACACCGTGATCAACCTCGCGGATTTGTTACCACTGCGCGAAGCTCGGCC 480
QY 481 AGGTTCCCACTCGGCGGAGCGCACGCTCAATGCTGTTGGGCGGTGCGGCTCCACT 540
XX

Db 481 GCGTTCCCACTGGGTGCGGATGCTACCTTATCAACGGGCTCGGGGTTTCCCCAGCAC 540
QY 541 CCCACGCGCGGCTTGTGATCAACGTCCAGCAGCGAAGCGCTACCGCTTCCGCTCTC 600
Db 541 ACGGCGCGGACCTCGAGTCAACGTCAACGAGGCAAGCGCTACCGTTTCCCGCTG 600
QY 601 GTTTCGATCTCGTGGACCCGAACACTACAGTTTCAGATCGACGGGCACAACTCTGACCCGT 660
Db 601 GTCTCCCTGCTGTGACCCCAACACAGTTCAGCATCGATCGATGATGACGATC 660
QY 661 ATCGAGGTCGAGGTCATCAACAGCCAGCCTCTCTTGTGCTGCTATCAGATCTTCGCG 720
Db 661 ATCGAGGTCGACTTCCATCAACTCGCAACCTCTGGTGTGTTGACTTCCATCCAGATTTTCGT 720
QY 721 GCGCAGCGCTACTCTCTTGTGTGAATGCAACAAACGGTGGCAACTACTTGGTCCGC 780
Db 721 GCGCAGCGTACTCTCTTGTGTGAATGCGGACGAGATGTCGGTAACACTTGGATTCGC 780
QY 781 GCGAACCCGAACCTCGGAACGGTTTGGTTCGCGGGGGGATCAACTTCCGCCATCTCTCGCC 840
Db 781 GCGAACCCCAACTTCGGCAACGTCGGATTTGCGGGTGGTATCAACTCGGCCATCTCTCGCC 840
QY 841 TACCAAGCGCACCACTCGCCGAGCCCACTAGCACCCAGACGACGTCGCGTATCCCGCTT 900
Db 841 TACGAGCGCGGACCCCGGTTGAGCCCCACACGACTCAGACTACGCGGACCAAGACCCCTG 900
QY 901 ATCGAGACGAACCTTGACCCCTCGCTCGCATGCTGCTGCTGGCAGCCGACACCCGG 960
Db 901 AAGGAGTTCGACTTGCACCCGCTCGCCACCATGGCTGTGCCGGTTCCCGCAGTCGCGGT 960
QY 961 GCGTCGACAAGCGGCTCAACCTCGGGTTTAACTTCAACGGGACCAACTTCTTTCATCAAC 1020
Db 961 GGTGTGACACGGCTATCAACATGGCTTCAACTTCAATGGTACCAACTTCTTTCATCAAC 1020
QY 1021 AACGCACTTTTCACGCGCGGACGCTCGCCGCTACTCTCTCAGATTCTGAGCGGTGGCAG 1080
Db 1021 GCGCGGAGGTTTGGCCCCACCGCTGCGCGGCTCTCTCCAGATCATCAGGCGGCCAG 1080
QY 1081 ACCGCAAGACCTGCTCCTCGAGGCTGTCTTACCCGCTCCCGGCCACATCCACATC 1140
Db 1081 AACGCCAGGATCTCCTCCGCTTGGCAGGCTCTACTCCCTCCCGTCAAAACGCGATATC 1140
QY 1141 GAGATCACGCTGCGCGGACCGCTTGGCCCGGGTGGACCGCCCTTCCACCTGCGAC 1200
Db 1141 GAGATCTGTTCCCTGCTACGGGGCTCTCCGGGTGCCCTCACCCCTTCCACTTGCAC 1200
QY 1201 GGTACGCGCTTCGCGGTGCTTCGACGCGGGGAGCAACACGTATTAACATCAACGACCG 1260
Db 1201 GGTACGCGCTTCGCGGTGCTTCGCTAGCGCTGGCAGCAGCGCTTACAACTACGACACCC 1260
QY 1261 ATCTTCCGCGAGCTGTGAGCAGCGGACCGCCCGCGGGGCGACAACTCAGGATCCGC 1320
Db 1261 ATCTTCCGCGAGCTGTGACGACGGGACGCTGCGGGCGGTGACAACTCAGCATCCGC 1320
QY 1321 TTTCAGACGCAACCCCGGCGCTGTTCTCCACTGCGCATGCTTCCACCTCGAC 1380
Db 1321 TTCCGCAACGCAACCCCTGCGCGGTGTTCTCCACTGCCACATCGACTTCCACTTGA 1380
QY 1381 GCGGGCTTCGCGATGCTGTTCGAGAGGACGTTGCGGAGCTGAAGCGGCGCAACCGGTT 1440
Db 1381 GCGGGCTTCGCGGTGCTGTTCGCGGAGGACATCCCGGAGCTGCGTGGCGCAACCCGTC 1440
QY 1441 CCGAAGGCTGTGTCGAGCTGTCCCGATCTACGAGGGGCTGAGCGAGGCTAACCG 1497
Db 1441 CCTCAGGCTATGCTGTGTCGCTATGACGCACTCGATGTCAGCAACCGACG 1497

RESULT 7
AAQ02671
ID AAX02671 standard; cDNA to mRNA; 1572 BP.
XX
AC AAX02671;
XX

DT 10-MAY-1999 (first entry)
DE T. versicolor laccase TV-1 cDNA from clone plac55.
XX
XX Laccase; TV-1; delignification; pulp; depolymerisation; waste water;
KW high-molecular-weight aggregates; delinking; waste paper; polymerisation;
KW aromatic compound; lignin; pulp bleaching; oxidising dye; activating dye;
KW pigment formation; organic synthesis; ss.
XX
XX Trametes versicolour.
XX DE19724039-A1.
XX 10-DEC-1998.
XX 06-JUN-1997; 97DE-1024039.
XX 06-JUN-1997; 97DE-1024039.
PR (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.
XX Pfaller R, Wich G;
XX WPI; 1999-036087/04.
XX
XX New DNA encoding Trametes versicolor laccase protein - used to e.g.
PT delignify pulp, depolymerise high molecular weight aggregates, delink
PT waste paper, polymerise aromatic compounds in waste water, activate
PT dyes and to couple organic compounds
XX
PS Claim 1; Page 13-15; 42pp; German.
XX
CC This invention describes novel laccase proteins isolated from Trametes
CC versicolor which can be used in methods for delignifying pulp,
CC depolymerising high-molecular-weight aggregates, delinking waste paper,
CC polymerising aromatic compounds in waste water (especially
CC lignin-containing waste water from pulp bleaching), oxidising dyes or
CC activating dyes for pigment formation, or in organic synthesis for
CC coupling aromatic compounds or for oxidising aromatic side chains.
XX
XX Sequence 1572 BP; 270 A; 555 C; 427 G; 320 T; 0 other;
SQ
Query Match 58.3%; Score 874.8; DB 20; Length 1572;
Best Local Similarity 74.1%; Pred. No. 4.8e-162;
Matches 1107; Conservative 0; Mismatches 387; Indels 0; Gaps 0;
4 ATCCGGCGGTGGCGAGCTTCGTCGGAACGCCCGCTCTCCGCGGAGCGGTTCTTCTT 63
DB 79 ATCCGGCGCTGTGCTCGACCTCAGCATCTCCAACGCGGTGTGCGCCGATGGCTTCT 138
64 CGGGATGCCATCGTGGTCAACGGCGGTGTCCTTCCCGCTCATCACGGGAAGGGA 123
DB 139 CGCGCGGGTGTGGGAAGGACAGGCTCCCGGGCTCTCATAGGGCCAGATGGC 198
124 GACCGCTTCCAGCTCAACGCTGTGCGACACCTTGACCAACACACAGCATGCTCAAGTCCACT 183
DB 199 GACCGTTTCCAGATCAATGTGGTCAACAAGCTGTGGAACACACATATGCTCAAGTCGACC 258
184 AGTATCACATGGCAGCGCTTCTCCAGGAGGACCAACTGGGCGAGGACGCGCGCTTC 243
DB 259 AGCATCCATGGCAGCGCTTCTCCAGAGGGTACGAAGTGGGCGGATGGCGCGCTTC 318
244 GTCAACAGTCCCTATTTGCTCCGGGCAATTCATTTCTGTACGACTTCCATGTCCCGGAC 303
DB 319 GTGAACAGTCCCGATCGGACTGGTCACTCTGTTCTTTACGACTTCCAGGTCCCGGAC 378
304 CAGCGAGGAAGTCTTGGTACCAAGTCAATGTGCTACGCAATATGTGACGAGGCGTCCGA 363
DB 379 CAGCGCGGAGCTTCTGGTACCAAGCATTTGTCTACCCAGTACTGTGACGGGTTGAGA 438
364 GGACCGTTCGTGCTAGGACCCCAAGGATCCGACGCGCCGCTACGATGTTGACAAC 423
DB 439 GGTCTCTCGTCTAGACCCGGAACGACCTCATGCCAGCCTCTACGACGCTGAGCAAC 498

QY 424 GAGAGCACGGTTCATACGTTTGACCGACTGTGTACCACACCGCTCCCGGCTCGGTCACAGG 483
DB 499 GATGACACCGTTCATCACCCCTCGCTGACTGTGTACCATACCGCTGCCAAGCTTGGGCGCGCC 558
QY 484 TTCCACTCTCGGCGGAGCGCACGCTCATCAATGGTCTTGGGCGGTGGCGCTCCACTCC 543
DB 559 TTCCCTCTGCTGTGATGGCGACGTTGATCAATGGTTCGGACGTACAGGGCGCACCC 618
QY 544 ACCGCGCGCTTGTGATCAACGCTCCAGCAGGAAAGCGTACCCTCCGCTCGCTT 603
DB 619 AACGCGGATCTCGCTGTCAATAGTGTACGACCGGAAAGCGGTACCCTTCCGCTCGGT 678
QY 604 TCGATCTCTGCGGACCGGAACTACACGTTTCAGCATTCGACGGGCAAACTCTGACGCTCATC 663
DB 679 TCGATGTCCTGGACCGCGGTACACGTTTCAGCATTCGACGACCACTCGATGACCATCATC 738
QY 664 GAGTGCACGGTATCAACAGCGGCTCTCTGTTGCACTCTATCCAGATCTTCCGCGCG 723
DB 739 GAGCGGACTCAGTCAACAAACAAACCGCTCGAGTGCATCGATCCAGATCTTCCGCGCG 798
QY 724 CAGGCTACTCTTGTGTTGAATGCAACCAACCGGTTCGGCAACTACTTGGGTCCGCGCG 783
DB 799 CAGGCTACTCTGCTGCTGGAGGAAACCAAGACGTCGGCAACTATTGGGTCCGCGCG 858
QY 784 AACCCGAACCTTCGGAACGGTTGGTTCCCGGGGGGATCAAACTCCGCCATCTCGGCTAC 843
DB 859 GACCCGCTGTTGGCACGAGGGCTTCGATGGGGGTATCAAACTCTCGGATCTCCGGTAC 918
QY 844 CAAGGCGCACGTCGCGGAGCGGCTACGACCCAGAGGAGTGGTGTATCCCGCTTATC 903
DB 919 GACACCGCTGCGCGAGCGGAGCGGACGACGAGGCGCACTCTCAAGAACCGTTGAAG 978
QY 904 GAGAGCACTTGCACCGCTCGCTCGGATGCTGCTGCGTGGCAGCGACACCGCGGCG 963
DB 979 GAGACGACCTTGAAGCTCTCGCTGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
QY 964 GTCCACAAAGGCGCTCAACCTCGCTTAACTTCAACGCGACCAAACTTCTTCAACAAC 1023
DB 1039 GTGCAAGGCGGATTAACCTTCGCTTCAACGGGTCCAACTTCTTCAACAACGCG 1098
QY 1024 GCGACTTTCAGCGCGCGACCGTCCCGTACTCTCTCAGATTCGTGAGGGTGGCGAGAC 1083
DB 1099 GCGACCTTCCAGCGCGCGACCACTCCCGTCTGCTGAGATCATAGCGGTGCCAGCT 1158
QY 1084 GCACAAGACCTGCTCCCTGCGAGGCTGTCTACCGCTCCCGGCGCACTCCACCATCGAG 1143
DB 1159 GCTAGCGACCTTCTCCCGTCCGCTGCGTGTACGCTTACGCGCTGCGCTGCGACTCGACCATCGAG 1218
QY 1144 ATCAGCTTCCCGCGGACCGCTTGGCGCGGCTGACCGCACCGCTTCCACCTGCACGCT 1203
DB 1219 CTCTCGTTCCCGCGGACTTACTGCTGCTCCCGGTGCCCGCCACCGCTTCCACTTGCACGCT 1278
QY 1204 CACGCTTCCGCGGTGCTTCGAGCGGCGGAGACCGCTATACCTACAGGACCGCGATC 1263
DB 1279 CACACTTCCGCGGTGTCGCGAGCGCGGCGAGCTGAGTACAACTACGACAAACCGCATC 1338
QY 1264 TTCCGCGACGTCGTGAGCACGGGCGACGCGCGCGGCGGAGCAAGCTCAGCATCCGCTTC 1323
DB 1339 TGGCGCGACGTCGTGACGACTGTACCCCTGACGCGGCGATAGCTCACCATTGCGCTTC 1398
QY 1324 CAGACGGACAACCCCGGCGCTGCTTCTTCCACTGCCACATCGACTTCCACTCGACGCG 1383
DB 1399 AGGACTGACAACCCCTGGCGCGCTTCTTCCACTGCCACATCGACTTCCACTTGGAGGCC 1458
QY 1384 GCTTTCGGATCTGTTGCGAGAGGAGCTTGGGACGTGTAAGGCGGCGCAACCGGTTCCG 1443
DB 1459 GCTTTCGCGGTGTCATGGCTGAAGACATCCCGGACCAAGCGCGCAACCGCTTCTCT 1518
QY 1444 AAGCGTGTGCGGACCTGTGCCGCTTACGACGCGGCTGAGCGAGGCTTAACAG 1497
DB 1519 CAGCGGTGTCAGACCTTGTGCCCATCTACGACGCGCTCGACGCGCTGAGGACGAG 1572

RESULT 8
AA02672
ID AAX02672 standard; cDNA to mRNA; 1572 BP.
XX
XX AAX02672;
XX
DT 10-MAY-1999 (first entry)
XX
XX T. versicolor laccase TV-1 cDNA from clone plac56.
XX
XX Laccase; TV-1; delignification; pulp; depolymerisation; waste water;
KW high-molecular-weight aggregates; delinking; waste paper; polymerisation;
KW aromatic compound; lignin; pulp bleaching; oxidising dye; activating dye;
KW pigment formation; organic synthesis; ss.
XX
XX Trametes versicolor.
XX OS
XX DE19724039-A1.
XX PN
XX 10-DEC-1998.
XX PD
XX
XX PF 06-JUN-1997; 97DE-1024039.
XX PR
XX 06-JUN-1997; 97DE-1024039.
XX PA
XX (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.
XX
XX Pfaller R, Wich G;
XX PI
XX WPI; 1999-036087/04.
XX DR
XX
XX PT New DNA encoding Trametes versicolor laccase protein - used to e.g.
PT delignify pulp, depolymerise high molecular weight aggregates, delink
PT waste paper, polymerise aromatic compounds in waste water, activate
PT dyes and to couple organic compounds
XX
XX Claim 1; Page 15-17; 42pp; German.
XX
XX This invention describes novel laccase proteins isolated from Trametes
CC versicolor which can be used in methods for delignifying pulp,
CC depolymerising high-molecular-weight aggregates, delinking waste paper,
CC polymerising aromatic compounds in waste water (especially
CC lignin-containing waste water from pulp bleaching), oxidising dyes or
CC activating dyes for pigment formation, or in organic synthesis for
CC coupling aromatic compounds or for oxidising aromatic side chains.
XX
XX Sequence 1572 BP; 269 A; 558 C; 429 G; 316 T; 0 other;
XX SQ

Query Match 58.1%; Score 871.6; DB 20; Length 1572;
Best Local Similarity 74.0%; Pred. No. 2e-161;
Matches 1105; Conservative 0; Mismatches 389; Indels 0; Gaps 0

QY 4 ATCGGCGCGGTGGCAGGCTCTGTCGGGAACGCCCGCTCGCCGAGCGGTTCTCTT 63
Db 79 ATCGGCGCGGTGGTCGACCTTACGATCTCCAATGGTGTGTCGCCGATGGCTCTCT 138
QY 64 CGGGATGCCATCGTGTGTCACGCGGTGTCCTTCCCGCTCATCACGGGAAGGGA 123
Db 139 CGCGCGCGGTGTCGGGAACGACGAGCTCCGGGCTCTCATCACGGGCGGATGGC 198
QY 124 GACCGGTTCCAGTCAACGTCGTCGACACCTTGACCAACACAGCATGCTCAAGTCCACT 183
Db 199 GACCGGTTCCAGATCAATGTGTCAACAAGTGTGCAACACACACCATGCTTAATCGACC 258
QY 184 AGTATCACTGGCAGCGGTTCTTCCAGGAGGACCAACTCGGCGAGACGACCGCGCTTC 243
Db 259 AGCATCACTGGCAGCGGTTCTTCCAGAAAGGCGAGAACTGGGGGAGCGGCGCTCGCTTC 318
QY 244 GTCACACGCTGCCCTATTGCTTCCGGGCAATTCATTCTGTACGACTTCCCATGTGCCCGAC 303
Db 319 GTGAACCAATGCCGATTCGACGGGCGCACTGTGTTCTTACGACTTCCAGGTGCCCGGAC 378

```
|||||
Db 1459 GCGTTCGCGTGGTCATGCGCTGAAGACATCCCGGACACCAAGGCGGACAAACCGCTGTCCT 1518
QY 1444 AAGGGGTGTCGGAGCTGTGCGCCGATCTACGACGGGCTGAGCGAGGCTTAACGAG 1497
|||||
Db 1519 CAGGCGGTGTCAGACCTTGGCCCAATCTACGACGCGCCCTCGAGGCTGACGACGAG 1572

RESULT 9
AAAT15599
ID AAAT15599 standard; DNA; 2880 BP.
XX
AC AAAT15599;
XX
DT 07-APR-1996 (first entry)
XX
DE Laccase-LCC2 gene.
XX
KW Laccase-LCC2; Polyporus pinsitus; Trametes villosa; primer;
KW polymerase chain reaction; PCR; signal peptide; cellulase;
KW Aspergillus oryzae; cDNA probe; Escherichia coli; plasmid pDSY19;
KW lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
KW cloning; basidiomycetes; ss.
XX
OS Polyporus pinsitus.
OS Trametes villosa.
XX
PH Key Location/Qualifiers
FT CDS 364..2492
FT /*tag= a
FT /product= Laccase-LCC2
FT /*note= "EC-1.10.3.2"
FT sig_peptide 364..423
FT /*tag= b
FT exon 364..543
FT /*tag= c
FT intron 544..592
FT /*tag= d
FT exon 593..661
FT /*tag= e
FT intron 662..715
FT /*tag= f
FT exon 716..835
FT /*tag= g
FT intron 836..899
FT /*tag= h
FT exon 900..1013
FT /*tag= i
FT intron 1014..1066
FT /*tag= j
FT exon 1067..1132
FT /*tag= k
FT intron 1133..1187
FT /*tag= l
FT exon 1188..1283
FT /*tag= m
FT intron 1284..1343
FT /*tag= n
FT exon 1344..1498
FT /*tag= o
FT intron 1499..1553
FT /*tag= p
FT exon 1554..1751
FT /*tag= q
FT intron 1752..1815
FT /*tag= r
FT exon 1816..1872
FT /*tag= s
FT intron 1873..1928
FT /*tag= t
FT exon 1929..2135
FT /*tag= u
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FT intron 2136..2195
FT /*tag= v
FT exon 2196..2492
FT /*tag= w
XX
PN WO9600290-A1.
XX
PD 04-JAN-1996.
XX
XX 15-JUN-1995; 95WO-US07536.
XX
PR 15-MAY-1995; 95US-0441147.
PR 24-JUN-1994; 94US-0265534.
XX
PA (NOVO ) NOVO NORDISK BIOTECH INC.
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
XX
XX WPI; 1996-068874/07.
XX P-PSDB; AAR90722.
XX
XX DNA constructs for expression of Polyporus laccase enzymes - for use
XX in e.g. lignin manipulation, juice mfr., phenol polymerisation and
XX phenol resin prodn
XX
XX Claim 5; Page 62-65; 137pp; English.
XX
XX The sequence encodes laccase-LCC2 (pI 5.95) from Polyporus pinsitus
XX (Trametes villosa). Polymerase chain reaction (PCR) amplification of
XX P. pinsutus cDNA using primers 3331 (AAT15603) and 3332 (AAT15604) gives
XX a 1500 bp fragment, which is joined to a signal peptide sequence
XX from a 43-kDa cellulase using primer pHD433 (AAT15605) and a pUC
XX forward primer in PCR. Clones are expressed in Aspergillus oryzae,
XX and a cDNA probe is obtained and used to screen a P. pinsutus
XX genomic library in Escherichia coli DH5-alpha, giving plasmid
XX pDSY19 (23GEN), with a 4-kb HindIII insert (NRRL B-21266).
XX Screening also results in isolation of LCC1 (AAT15598) and LCC3-LCC5
XX (AAT15600-T15602), which encode different laccases produced by P.
XX pinsutus. The laccases may be used to polymerise lignin or
XX lignosulphonates, to depolymerise Kraft pulp, to oxidise dyes or
XX precursors, in hair dye compositions, or to polymerise or oxidise a
XX phenolic or aniline compound. These new laccases are well-expressed
XX in Aspergillus spp. (with vector integration in the genome), in
XX contrast to previous basidiomycete laccases, which give low yields
XX of recombinant enzyme.
XX
XX Sequence 2880 BP; 547 A; 908 C; 793 G; 632 T; 0 other;

Query Match 51.5%; Score 771.8; DB 17; Length 2880;
Best Local Similarity 70.7%; Pred. No. 6.6e-142;
Matches 1463; Conservative 0; Mismatches 37; Indels 569; Gaps 10;

QY 1 GCCATCGGCGCGTGGCGAGCGCTGCTGCGGAACGCCCGCTCCCGGAGCGGCTTC 60
|||||
Db 424 GCCATCGGCGCGTGGCGAGCGCTGCTGCGGAACGCCCGCTCCCGGAGCGGCTTC 483
|||||
QY 61 CTTGGGATGCCATCGTGGTCAACGGCGGTGCTCCCGCTCATCACCGGGAGA-- 118
|||||
Db 484 CTTGGGATGCCATCGTGGTCAACGGCGGTGCTCCCGCTCATCACCGGGAGAAG 543
|||||
QY 119 -----AGGGAGACCGGCTT 131
|||||
Db 544 GTCGGCGGTGTTGCTGCTGCTCTACTCTCTTGTCTACAGCGATCTACAGGGAGACCGGCTT 603
|||||
QY 132 CCAGCTCAACGTCGTCGACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATC-- 189
|||||
Db 604 CCAGCTCAACGTCGTCGACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATC 663
|||||
QY 190 -----CACTGGCA 197
|||||
Db 664 AAGTGTGACGATCCGAATGTGACATCAATCGGGGCTAATTAACCGCGGCACAGCACTGGCA 723
|||||
```


XX Pfaller R, Hessing J, Van Den Hondel C, Van Gorcom R;
XX WPI; 1999-633742/54.
XX
XX An expression system for the production of proteins in filamentous
XX fungi -
XX
XX Claim 8; Page 50-53; 67pp; German.
XX
XX This invention describes a novel expression system for the production
XX of a protein in a filamentous fungus which comprises a Trametes or
XX Polyporus host organism, a DNA vector containing a positive selection
XX marker and a DNA vector containing a gene of interest controlled by an
XX active genetic regulation element in the host organism. The fungi are
XX useful for the production of hydrolytic enzymes, e.g. cellulases,
XX hemicellulase and lipases or oxidoreductases, e.g. lignin peroxidase,
XX mangan peroxidase, laccase, cellobiose-chinon oxidoreductase or
XX cellobiose-oxidase. This sequence represents the laccase I nucleic acid
XX sequence isolated from Trametes versicolor.
XX
XX Sequence 7986 BP; 1698 A; 2404 C; 2107 G; 1777 T; 0 other;
XX
XX Query Match 50.4%; Score 755.4; DB 20; Length 7986;
XX Best Local Similarity 70.2%; Pred. No. 1.1e-138;
XX Matches 1449; Conservative 0; Mismatches 51; Indels 563; Gaps 10;
XX
QY 1 GCCATCGGGCGGTGGCGAGCCTCGTCTCGCGAAGCCCGCTCTCGCCGACGGCTTC 60
DB 1253 GCCATCGGGCGGTGGCGAGCCTCGTCTCGCGAAGCCCGCTCTCGCCGACGGCTTC 1312
QY 61 CTTCCGGATGCATCTGTTGTCAGCGGTGGTCCCTTCCCGCTCATCACCGGGAAGA-- 118
DB 1313 CTTCCGGATGCATCTGTTGTCAGCGGTGGTCCCTTCCCGCTCATCTACTGGGAAGA 1372
QY 119 -----AGGAGACCCCTT 131
DB 1373 GTCGGCGTGTGTTGTCGCTTACTCCTTTACTGACAGGATCTACAGGAGACCGCTT 1432
QY 132 CCAGCTCAAGTCTGTCAGACACTTGAACCAACACAGCATGCTCAAGTCCACTAGTATC-- 189
DB 1433 CCAGCTCAAGTCTGTCAGACACTTGAACCAACACCATCCATGCTCAAGTCCACTAGTATC 1492
QY 190 -----CACTGGCA 197
DB 1493 AAGTGTGACGATCCGAATGTGACATCATCGGGGCTAATTAACCGCGACAGCATGGCA 1552
QY 198 CGGCTTCTCCAGCGAGCACCACCTGCGGAGACGGACCGCGTTCGTCACAGTGGCC 257
DB 1553 CGGCTTCTCCAGCGAGCACCACCTGCGGAGACGGACCGCGTTCGTCACAGTGGCC 1612
QY 258 TATTGCTTCGGGCAATTCATTCTGTACGACTTCCATGTGCCGACGAG----- 307
DB 1613 TATTGCTTCGGGCAATTCATTCTGTACGACTTCCATGTGCCGACGAGTAAAGCA 1672
QY 308 -----CAGGAA 313
DB 1673 GTCTTTTGTGTGATCCCTCGTGTGATGCAATGTTCTCATGTCTCCGACGTGATCGAGGGA 1732
QY 314 CGTTCGTGTACACAGTCACTGTCTAGCAATGCTGAGCGGCTGCGAGGACCGTTCG 373
DB 1733 CGTTCGTGTACACAGTCACTGTCTAGCAATGCTGAGCGGCTGCGAGGACCGTTCG 1792
QY 374 TCGTGTACGAGCCCAAGGATCCGACGCCAGCCGCTACGATGTTGCAAC----- 423
DB 1793 TCGGTGTACGAGCCCAAGGATCCGACGCCAGCCGCTACGATGTTGCAACCGGTACGTGG 1852
QY 424 -----GAGAGCAGGTCATCAC 440
DB 1853 CCAGGAGTATATCACACAGCATGCGTTGACGTTCGGGCCAACAGACAGCAGCGTTCATCAC 1912
QY 441 GTTGACCGACTGTGTACACACCGCTGCGCGCTCGGTTCGCGAGTTC----- 488
DB 1912 GTTGACCGACTGTGTACACACCGCTGCGCGCTCGGTTCGCGAGTTC----- 488

DB 1913 GTTGACCGACTGTGTACACACCGCTGCGCGCTCGGTTCGCGAGTTCGCGTAAAGTCGCA 1972
QY 489 -----ACTCGGCGGAGCGCA 505
DB 1973 TGGATTAGTTTTTACGGATTATTTGCTTATGTTGCTCGTAGACTCGGCGGAGCGCA 2032
QY 506 CGCTCATCAATGTTGTTGGCGGTGCGGCTCCACTCCACCGCGCGCTGCTGTGATCA 565
DB 2033 CGCTCATCAATGTTGTTGGCGGTGCGGCTCCACTCCACCGCGCGCTGCTGTGATCA 2092
QY 566 ACCTCCAGCAGCGGAAGC----- 583
DB 2093 ACCTCCAGCAGCGGAAGCGGTGAGCATTTCTTGTGATGCCATTTCAATGCTTAAATGA 2152
QY 584 -----GCTACCGCTTCCGCTCGTTCGATCTCGTCGCGACCGCAACTA 626
DB 2153 CCTATCCGCGCAGCGAGCTACCGCTTCCGCTCTGTTTTCGATCTCGTCGCGACCGCACTA 2212
QY 627 CAGCTTCAGCATCGACGGGCACAATCTGACCGTCTCATGAGTTCGACGATATCAACAGCA 686
DB 2213 CACGTTTCAGCATCGACGGGCACAATCTGACCGTCTCATGAGTTCGACGATATCAACAGCA 2272
QY 687 GCCTCTCTTGTGCTGACTCTATCCAGATCTTGCCTCGCGCGAGCGCTACTCTTTGT- 740
DB 2273 GCCTCTCTTGTGCTGACTCTATCCAGATCTTGCCTCGCGCGAGCGCTACTCTTTGTGATG 2332
QY 741 -----GTTGAATGCA 751
DB 2333 TCCTGCTCTTGTGCTTCCAAAGTGGCTCGCTCACCCTATCTTTAGTTGAATGCA 2392
QY 752 ACCAAAGGTGCGCAACTACTTGGTTCGCGGAAACCCGAACTTCGGAACGGTTGGGTTG 811
DB 2393 ACCAAAGGTGCGCAACTACTTGGTTCGCGGAAACCCGAACTTCGGAACGGTTGGGTTG 2452
QY 812 CCGGGGATCAACTCCGCTATCCGCTCTGCTACCAAGCGCACCACTGCGCGAGCCCACTA 871
DB 2453 CCGGGGATCAACTCCGCTATCCGCTCTGCTACCAAGCGCACCACTGCGCGAGCCCACTA 2512
QY 872 CGACCCAGAGACGCTCGGTGATCCGCTTATCGAGAGAACTTCACCCCTCGCTCGCA 931
DB 2513 CGACCCAGAGACGCTCGGTGATCCGCTTATCGAGAGAACTTCACCCCTCGCTCGCA 2572
QY 932 TGCCTGT----- 938
DB 2573 TGCCTGTGTTAGTTCCTTTTCAATATATATGACCGCTGCGGAGTCAACCGCGCT 2632
QY 939 -----GCTGCGACCGGACACCGGGGCTGACAAAGCGCTCAACCTCGCGTT 990
DB 2633 CCTATCCAGCTGCGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2692
QY 991 AACTTC----- 996
DB 2693 AACTTCGTGAGTGTCTATACCGCCCAATTTGGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2752
QY 997 --AAGCGCACTTCTTCAATCAACAGCGACTTTCACCGCGCGGACCGTCCCGGTAC 1054
DB 2753 AGAAGCGCACTTCTTCAATCAACAGCGCTTTCACACCGCGAGTCCCGGTG 2812
QY 1055 TCCTCCAGATTTCTGAGCGGTGCGCAGACCGCACAAAGACTCTGCTCCCTGCGAGCTGCTGCT 1114
DB 2813 TCCTCCAGATTTCTGAGCGGTGCGCAGACCGCACAAAGACTCTGCTCCCTGCGAGCTGCTGCT 2872
QY 1115 ACCGCTCCCGGCGCACTTCCACCATCGAGATCACGCTGCGCGACCGCTTGGCCCGG 1174
DB 2873 ACCGCTCCCGGCGCACTTCCACCATCGAGATCACGCTGCGCGACCGCTAGCCCGAG 2932
QY 1175 GTGACCGCAGCCCTTCCACCTGACCGT----- 1203
DB 2933 GCGCGCGCAGCCCTTCCACCTGACCGTGTGACGCTCCCGCTTCTTCTTCTTCTTCTTCTTCTTCT 2992
QY 1204 -----CAGCGCTTTCGCGGTGCTGCGAGCGCGGGAGCA 1237
DB 2993 CAAGTGTACGCTCCAGCCCTCTAGCAGCGGTTTCGCGGTGCTGCGAGCGCGAGCAGCA 3052


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Qy 1046 TCCGGTACTCTCCAGATTGTCAGCGTGGCGAGACCGCACAAAGAACTGCTCCCTCGAG 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1206 CCCCTGCTCTCCAAATCTCTCAGAGAGCTCGATGCTGTCATCGCTTCTTCTCCG 1265

Qy 1106 CCTCTGTCTACCCGCTCCCGCCACCTCCACCATCGAGATCACTGCTGCCGCGACCGCT 1165
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1266 GTAGCATTTAGGAGCTGAAGCTAACAAAGTTGTGAAATCTCGATACCTGCG-----C 1319

Qy 1166 TGGCCCGGGTGCACCGCACCCCTTCACCTGCACGCTCAGCGCTTCGCGTCTGTCGCA 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1320 TGGTGTGGGGGACCCCATCCGTTCCATCTTCACGCTCACACCTTCGACGTTATTAGGA 1379

Qy 1226 GCGCGGGAGACACCATATTAATACAAACACCGCATCTTCGCGAGCTCGTGTGACGCG 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1380 GTGCGGGTTCACCTACGCTACAACTTCGACACTTCGCGCGCGCGGCTGTCAACACTG 1439

Qy 1286 GCAGCCCGCGCGGGGACAACTGACGATCCGCTTCCAGACGGAACCCCGGGCGT 1345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1440 GCA---CTGATGCGAAGCAACGCTCACTATTCGCTTCGTGACCGCAACCCAGGCGCGT 1496

Qy 1346 GGTTCCTCCACTGCGACATCTCCACCTCGACGCGGGCTTCGCGATCGTGTTCGCG 1405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1497 GGTTCCTCCACTGTCATATTGATGGCATCTCGAAATGGTCTCGCTGCTGCTTTTCGCG 1556

Qy 1406 AGGACGTTGCGGAGCTGAAGCGGCGGAACCGGTTCCGAAAGCGTGTGCGACCTGTGCC 1465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1557 AAGACGTGACATCATATTTCGGCCCC-----ACCTGCGCGCTGGGACGACTTGTGCC 1607

Qy 1466 CGATCTAGGAGCGCTGAGCGAGCTACACAGTGA 1500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1608 CCATATATGATGCTTTGAGCGACAAACGACAAAGGA 1642
```

RESULT 12

AAA57439

ID AAA57439 standard; cDNA; 1722 BP.

XX AC

XX AC

XX AC

DT 03-OCT-2000 (first entry)

XX cDNA sequence encoding a phenol oxidising enzyme.

XX Phenol oxidising enzyme; detergent; colour modification; dye; tannin;
KW carotenoid; anthocyanin; textile; cleaning; pulp; paper; food;
KW wood processing; ss.
XX Pleurotus ostreatus.

XX Key Location/Qualifiers
FH 59..1660
FT CDS

FT /*tag= a

FT /trans_except= (pos: 917..919, aa: Val)

FT /product= "phenol oxidising enzyme"

XX WO200037601-A2.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US30869.

XX 23-DEC-1998; 98US-0221275.

XX (GENV) GENECOR INT INC.

XX Borneman WS, Graycar TP, Bodie EA, Winetsky D;

XX WPI; 2000-475524/41.

XX P-PSDB; AAY93953.

XX Detergent composition for modifying colour associated with dye or a
PT coloured compound in a sample comprises a phenol oxidising enzyme
obtainable from *Pleurotus ostreatus*

XX Claim 4: Fig 3; 25pp; English.

XX The present sequence encodes a phenol oxidising enzyme, from *Pleurotus*
CC *ostreatus*. The sequence is cloned, and used to produce a protein.
CC which is then used in the detergent compositions of the invention.
CC These detergent compositions are capable of modifying the colour
CC associated with a coloured compound at alkaline pH. The detergent
CC compositions are useful for modifying the colour associated with the
CC dye or coloured compounds such as tannins, carotenoids and anthocyanins
CC in a sample by contacting the sample at alkaline pH. They are useful in
CC textile, cleaning, pulp and paper applications and also in food and
CC wood processing industries.

XX Sequence 1722 BP; 364 A; 513 C; 380 G; 465 T; 0 other;

Query Match 34.6%; Score 519; DB 21; Length 1722;
Best Local Similarity 63.6%; Pred. No. 1.6e-92;
Matches 900; Conservative 0; Mismatches 485; Indels 30; Gaps 6;

Qy 92 TCCCTTCCCGCTCATCACCGGGAAGGAGGACCGCTTCCAGCTCAACGTCGTCGACA 151
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 252 TTCTCGGGTCTCGTTCAGGAAACAAGGCTGATCACTTCCAGCTGAACGTCGTCATC 311
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 152 CTTTGACCAACACAGCATGCTCAAGTCCACTAGTATCCACTGGACGGCTCTTCTCCAGG 211
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 312 AATTATCGGACACGACCATGTTGAAGACGACGATTCATTTGGCAGCGTTTCTTCCAAG 371
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 212 CAGGACCAACTGGCGACGAGCGCGGTCGTCACACGCTGCCTATTCGTTCCGGGC 271
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 372 CCGGATCTTCGTGGGCTGATGGTCCCGCTTTCGTGACCAATGCCCGCTCGCCCTCGGG 431
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 272 ATTCATTTCTAGCACTTCCATGTGCCGACGAGGAGGAAACGTTCTGGTACCACGATC 331
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 432 ATAGTTCCTGTACAATTCATGTACCAGACCAAGCTGGAACATTTTGGTATCACTGCG 491
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 332 ATCTGTCTACGCAATACGTGACGGGTGCGGAGGACGCTTCGTCGTGTACGACCCGAGG 391
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 492 ATCTTTCACCCCAATATTGTGACGGCTCAGAGGACCAATTTGTGTATACGACCCCTCG 551
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 392 ATCCGACGCCGCGCTACGATGTGACAACGAGAGACGCTCATCATCTTGACCGACT 451
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 552 ATCCGCACTTGAGTTTATACGATATTGACAACGCTGACACGCTCATTTAGCTTGAGGAT 611
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 452 GGTACCAACACGCTGCCGCGCTCGGTCCAGGTTCCCACTCGGCGCGGACCGACGCTCA 511
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 612 GGTATCATATCGTGCCCTCAAAACGCGCGATCC---CACCCGCGATAGTACTCTCA 668
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 512 TCAATGGTCTTGGGCGGTGCGGCTCCACTCCACGCGCGCGCTGCTGTGATCAACGCTC 571
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 669 TCAATGGTAAAGGTGTTTACGCGGGGCGGCTACCTCCCTTTTGTCCATCATCAACGCTG 728
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 572 AGCAGGAAAGCGTACCGCTTCGTCGTTTCGATCTCGTGGACCGGACCGACTACAGT 631
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 729 AAGCAACAAGCGCTATCGTTTCAGACTGTCTATTGCTTTCGATCCTTAATTTACAGT 788
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 632 TCAGCATCGAGGGCACAATCTGACCGTCACTCGAGGTGAGGATCAACAGCCAGCCTC 691
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 789 TCTCGATCGACGCTCACTCTTTGCTCGTCATTGAAGCAGATGCTGTCAACATTTACCCA 848
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 692 TCCCTGTGCACTCTATCCAGATCTTTCGCGCGGCGGCGCTACTCTTGTGTGTAATGGA 751
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 849 TCACGCTGGATAGTATTCAGATCTTTCGCTGGCCACGCTACTCTCTTCTTGTGCTG 908
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 752 ACCAAGCGTGGCAACTACTGGGTCCGCGGGAACCCGAACCTTCGGAACGGTTGGTTCG 811
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 909 ATCAGACCATTTGGCAATTTACTGGATTCGCGGGAATCTTAACTTGGGATCGACTGTTTCG 968
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 812 CCGGGGGATCAACTCCGCCCATCTTCGCTGCTACCAAGGCGGACCACTGCGCGGACCCACTA 871
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 969 ACGGTGGTATCAATTCGCGCTATCTTCGATATGCTGGTGGCCACTGAGGATGACCCCTACTA 1028
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 872 CGACCCAGACGCTGCGGTGATCCCGCTTATCGAGACGAACCTTGCACCCCTCGCTCGCA 931
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 841 TACCAGGCGCAGTCCCGAGCCCACTACGACCCAGACGAGTGGTGATC----- 894
Db 991 TATCGGCGCTCTCTCCGAGCCGCTGAGTGCATACGAGCCGCTCTCTCTTGC 1050
QY 895 CCGCTTATCGAGCAACATTGACCCCTCGCTCGCATCCCTGTGCTGGCAGCCGACA 954
Db 1051 CTTTGTGGAGACCGCCCTCGCTCTCGAGAACCTTGGCGCCTGGTCTCCGCCAG 1110
QY 955 CCGGGGGCGTGGCAAGCGCTCAACCTCGCGTTTAACT-----TTCAACGGCACCAAC 1008
Db 1111 CAAGGGGAGCGAGTGAACATCAACCTCGGATGACCTTACGCTGACCCATTCAG 1170
QY 1009 TTCTTCATCAACAGCGACTTTTACGCGCGCGAGCCGCTCCCGGTACTCTCCAGATTCTG 1068
Db 1171 TACAGGGTGAAGCGCGCATTCATTCGCGGAGTCTCGCGGTGTGTCGAGGTGATG 1230
QY 1069 ACGGTGGCAGACCGCACAACTGCTCCCTGAGGCTCTGTCTACCGCTCCGGCC 1128
Db 1231 AGCGGAGCGGTACTGCGCAGGAGTGTTCGGAAGGAGCGGTGTACACGCTACCGCC 1290
QY 1129 CACTCCACCATCGATCACTGCGCGCGACCGCTTGGCCCGGGTGCACCGCACCC 1188
Db 1291 AACCAGCGTTGAGATATCGATAC-----CCGGCGGAGTGTGGAGCCCTCATCT 1344
QY 1189 TTCCACCTGACCGGTCAAGCCTTCGCGGTTCGCGAGCGGGGAGCACACGATATAC 1248
Db 1345 TTCCATTTGACGGGACATAGTTTCGAGTGTTCGCGCGGGGAGCAGGACTACAA 1404
QY 1249 TACAAGACCCCATCTTCGCGACGCTGTGAGCAGCGGCGACCCCGCGGGGACAA 1308
Db 1405 TACGGAATTCGATTCGCGGAGCTGTGTCACACGCGGCTTG-----GCTGCTGACAA 1458
QY 1309 GTACGATTCGCTTCAGACGACAAACCGCGCGGTGTCTCTCCACTGCGCACATCGAC 1368
Db 1459 ACTAGATTCGATTACGACACAAATTCGCGGCGCTGGATCTTCATTCGATATGAC 1518
QY 1369 TTCCACCTGCGCGCGGTTCGCGATGCTGTTCGAGAGGAGTTCGCGACGTGAAGCG 1428
Db 1519 TGGCACCTCGACATCGGTCTCGCGCTGTGATGGCAGAGGAC---ACGATGGTATGG 1575
QY 1429 GCGAACCGGTTCGAAGCGGTGCTGCGACCTGTCGCGATCTAGACGGGTGAGCGAG 1488
Db 1576 CAGTCCGTACGCCAACTGCATACAGTATCTCTGCCAAGTACGACGCGTGTCTGAC 1635
QY 1489 G 1489
Db 1636 G 1636

RESULT 14
ID ABK50850
XX ABK50850 standard; DNA; 1801 BP.
AC ABK50850;
XX
XX
XX 30-JUL-2002 (first entry)
XX
XX DNA encoding Lentinula edodes protein with laccase activity #1.
XX Laccase; enzyme; gene; ds.
XX Lentinula edodes.
XX
XX
XX Key location/Qualifiers
XX CDS 47..1603
XX /*tag= a
XX /product= "Lentinula edodes protein with laccase
XX activity"

JP2002065282-A.

05-MAR-2002.

XX

PF 04-SEP-2000; 2000JP-0267473.
XX
PR 04-SEP-2000; 2000JP-0267473.
XX
PA (IWAT-) IWATE KEN.
XX
XX WPI; 2002-377662/41.
DR P-PSDB; AAU96688.
XX
XX New proteins derived from Lentinula edodes for use in providing laccase
PT enzyme activity -
PS
XX Claim 3; Page 13-15; 30pp; Japanese.
XX
XX The invention describes novel proteins derived from the species
CC Lentinula edodes and having laccase enzyme activity. This sequence
CC encodes a Lentinula edodes protein having laccase activity.
XX
SQ Sequence 1801 BP; 419 A; 480 C; 383 G; 519 T; 0 other;

Query Match 34.0%; Score 509.4; DB 24; Length 1801;
Best Local Similarity 61.1%; Pred. No. 1.2e-90;
Matches 917; Conservative 0; Mismatches 566; Indels 18; Gaps 5;

QY 1 GCCATCGGCGGTGGCGAGCCTCGTCGCGAAGCGCCCGCTCTCGCCCGACGGCTTC 60
Db 101 GCCATCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 160
QY 61 CTTTCGGGATGCCATCGTGGTCAACGGCGTGGTCCCTTCCCGCTCATCACCGGGAAGA 120
Db 161 AACCGCTCTGGTGTCTCTGCTGAGGCGCTTCTCTGGACCACTCATACGGGTAAACA 220
QY 121 GGAGACCGCTTCCAGCTCAACGCTGCTGACACCTTGACCAACACAGCATGCTCAAGTCC 180
Db 221 GCGCAATTTCCAGATCAATGTGATGATGATGATGATGATGATGATGATGATGATGAT 280
QY 181 ACTAGTATCCACTGGCAGCGCTTCTTCCAGGCGAGGACCACTGGGCGACGAGCCCGG 240
Db 281 ACTTCGATTCATTGGCAGCGCTTCTTCCAGAAACACCACTGGGCGACGAGCA 340
QY 241 TTCGTCAACAGTGGCTTATGCTTCCGGGCAATTCATTTCTGTAGACATTCATGTCGCC 300
Db 341 TTCGTGAATCAATGCTTATCGCGCGAATGATCTCTCTGTACAAATTCATGTTCCG 400
QY 301 GACGAGGAGGAACCTTCTGTACACAGTCTGTCTACGCAATCTGTCTGACGCGCTG 360
Db 401 GACGAGTGGAGCTTCTGTGTATCACAGTCACTATCCACTCATATTCGATGATG 460
QY 361 CGAGACCGTTCGTGTACGACCCCAAGGATCCGACGCGCGCGCTACGATGTTGAC 420
Db 461 CGTGACCGCTTGTGTGTATGACCCCTCAAGATCCATAGCTGACCTATACGAGTTGAT 520
QY 421 ACGAGACGAGGTATCATCGTTGACCGACTGTTACACACCGCTGCGCGGCTCGGTGCC 480
Db 521 GATGATCAACTGTCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 580
QY 481 AGGTTCCACTCGGCGGACGCGCTCATCAATGCTTGTGGGCGTTCGCGCTCCACT 540
Db 581 GCTGTTCGACCT---CGGACCGCACTCTCATCAATGGCTAGGAGATCCCTCAACGGT 637
QY 541 CCCACCGCGCGC---TTGCTGTGATCAACGCTCCAGCAGCGGAAGCGCTACCGTTCCGT 597
Db 638 CCAGCGGATGACCCCTTGTCTGTAGTCAATGCTGAGGCTAGTGTGCTGCTGCTGCTGCT 697
QY 598 CTCGTTTCGATCTCGTGGACCGCACTACAGTTTACGATCGACGCGGCGACATCTGACC 657
Db 698 TTGGTGTGATATCTGTGATCCGAACTTCTGTTTTCGATGACGCGGCGACCTTTACT 757
QY 658 GTCATCGAGGTGCGCGGTATCAACGCGAGCTCTCTCTGTGCTGCTCATCATCATCTTC 717
Db 758 GTCATTGAAGCTGATGGTGTAAATCATGAACCCATGTCGCTGATTCATCATCAGATTTC 817
QY 718 GCCGCGCAGCGCTACTCTCTTGTGTTGAATGCGAAGCAACGCGTGGCAACTACTGGGTC 777


```
Db 818 GCTGCTCAACGATACTCGTTTCATCTCACTGCAAACTCAAACTGCTGATAATATTATGGATC 877
QY 778 CGCGGAACCCGAACTTCGACGGTTGGGTTGCGCGGGGGATCACTCGGCATCCTG 837
Db 878 CBTGCCATCCTAACACGGACATACCGGCTTCGCTGGGGGTATAACACGGCGATCTG 937
QY 838 CGCTACCAAGCGCACAGTCGCGAGCCCACTACGACCCAGACGAGTCGGTGATCCCG 897
Db 938 CATTATTCTGGCGCCCTGTTGCTGATCGGTCACTACCCA---GACTTCTGCCAACCTT 994
QY 898 CTTATCGAGACGAACCTTGACCCCTCGCTCGCATGCTGCTGCTGGCAGCCCGACACCC 957
Db 995 CTACGGAACACAGCCTTGTCGCGGTGAAATCCCGGTGCTCTGGAATGCAACTGCT 1054
QY 958 GGGGGCTCGACAAGCGCTCAACGCGCTCAACGCTTTAACTTCAACGCGCACCAACTTCTTCATC 1017
Db 1055 AACGGCTAGATGTTGACTTGAATCGTCTTATCATTTGTTGGAGGACGGTTCGAGATT 1114
QY 1018 AACACGCGACTTTCACGCGCGCGACCGTCCCGGTACTCCTCAGATTCGTAGCGGTGCG 1077
Db 1115 AAGGGGTATCCTTTGTACCCCTACAGTCCCTGTCTTACTTCAAAATTCACGCGGAGCC 1174
QY 1078 CAGACGCAACAGACTGCTCCCTGCGAGGCTGTCTACCGCTCCCGGCCCACTCCACC 1137
Db 1175 ACTACAGACCGCAACTTCTACCCAGTGGCTCTGTTTATACATTGCCCTTGAATTCGGTC 1234
QY 1138 ATCAGATCATCGTCCCGACCGCTTGGCCCGGGTGCA---CGCACCCCTTCCAC 1194
Db 1235 ATCCAGTTGAGCTTTAATACGGTTGCAGTTGCAGAGTTGGAGGTCTCTCATCCATTCAT 1294
QY 1195 CTGACGGTTCACGCTTCGCGGTCTGTCGAGCGCGGGGAGCAGCAGGTATACATCAAC 1254
Db 1295 CTTACGGGACACATTTGACGTGGTCCGAAAGTCCCGAAGTACCGAGTATAACTATATC 1354
QY 1255 GAGCCGATCTTCGCGACGCTGTCGAGCAGCGGCGACGCGCGCGGCGACACGTCACG 1314
Db 1355 AACCTCCGCGAGGATGTCGTCTACTGGT-----GCAGTACTGACATGTAACC 1408
QY 1315 ATCCGCTTCAGAGGACAAACCCCGGCGGTGTTCTCTACCTGCCACATCGACTTCCAC 1374
Db 1409 ATTGCTTTTACTACTGATATAATGCTGACCATGTTCTTCTACCTGTACATAGATGGCAT 1468
QY 1375 CTGACGCGGGCTTCGCGATCGTTCGAGAGGAGGTTTCGCGACGTGAAGCGCGGAAC 1434
Db 1469 CTGGAAGCTGGTTTGCATATGTTTTCGTGAGGATGACCGGACGTCGCGCGCGTTAAT 1528
QY 1435 CCAGTTCCGAAGCGGTGCGGACCTGTGCGCGATCTACGACGGGCTGAGCGAGGCTAAC 1494
Db 1529 CCGTCCCGACGCTTGGAAATCACTTTGCCCAACTATGATGCTTTGACCCCTGCACAA 1588
QY 1495 C 1495
Db 1589 C 1589
```

RESULT 15

AA67137
ID AAT67137 standard; cDNA; 1170 BP.

XX

AC

XX

DT

XX AAT67137;

XX

22-JUL-1997 (first entry)

XX

DE Coprinus cinereus lcc2 partial cDNA.

XX

KW Benzenediol: oxygen oxidoreductase; laccase; lignin; Kraft pulp; dye;

XX

XX fungus; polymerase chain reaction; papermaking; ss.

XX

OS Coprinus cinereus (strain IFO 8371).

XX

PN W09708325-A2.

XX

PD 06-MAR-1997.
XX
PF 20-AUG-1996; 96WO-US13728.
XX
PR 25-AUG-1995; 95US-0002800.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO-NORDISK AS.
PI Brown KM, Halkier T, Kauppinen S, Yaver DS;
XX WPI; 1997-179282/16.
XX
XX New laccase from Coprinus strains - useful for polymerising lignin,
PT depolymerising Kraft pulp, oxidising dyes and their precursors, etc.
PS Example 5; Page -: 62pp; English.
XX
CC The present sequence encodes a partial cDNA of lcc2, isolated from
CC Coprinus cinereus strain IFO 8371, starting in exon 3. The lcc2
CC polypeptide is used to polymerise a lignin or lignosulphate in solution;
CC for in situ depolymerisation of Kraft pulp; for oxidising dyes or their
CC precursors; particularly to prevent dye transfer between fabrics and in
CC hair dyeing) and for polymerising or oxidising phenolic compounds (e.g.
CC to precipitate phenolics from fruit juices to give a more stable
CC product). It can also be used for soil detoxification. Use of the
CC polypeptide avoids the need to use chlorine for lignin depolymerisation.
CC It has better activity than known laccases under the alkaline conditions
CC usually encountered in papermaking processes.
XX
SQ Sequence 1170 BP; 228 A; 384 C; 264 G; 294 T; 0 other;

Query Match 31.5%; Score 472.6; DB 18; Length 1170;
Best Local Similarity 65.0%; Pred. No. 1.9e-83;
Matches 770; Conservative 0; Mismatches 394; Indels 21; Gaps 4;

QY 190 CACTGGCAGCGCTTCTCCAGGAGGACCAACATGGCGACAGCAGCCGCTTGGTCAAC 249
Db 1 CACTGGCAGCGCATTTTCAAAGGGGACTGCCCTGGGCTGATGGTCTGGCGTCAAC 60
QY 250 CAGTGCCTATTGCTCCGGGCATTTCTGTACCACTTCCATGTGCCGACGAGCA 309
Db 61 CAATGCCCTATTTCCCGAGGCGATTCGTTCTGTACAAGTTCCAGGCTCTTAAACAAGCC 120
QY 310 GGAACGTTCTGGTACCACTCATCTCTACGCAATACGTGTACGGGCTGCGAGGACCC 369
Db 121 GGTACTTCTGGTACCACTCCCATACGAATTCGAATATTGTGACGGTTTGGCTGGGCT 180
QY 370 TTGCTGCTGTACGACCCCAAGGATCCGACGCGCGCTACGATGTTGACACGAGAGC 429
Db 181 ATGGTCTATATGACCCGATCGACCCACATCGCAACTTGTATGACATTGACACGAGGCC 240
QY 430 ACGGTCTACAGTTGACCGACTGGTACCACTGCCGCGCTCCCGGCTCGGTCACGAGTTCCCA 489
Db 241 ACGATCATTAAGCTCGCAGACTGGTATCACGTCCCTGC---TCCCTCTGCAGGTTCTGTT 297
QY 490 CTGCGCGCGGACGCGCAGCTCATCAATGGTCTTGGGCGGCTCGGCTCCATCCACCGCC 549
Db 298 CCCACCCAGATTCCAGCTTATCAACGGTAAGGGCGGATGCTGGTGGCCCTTACCGTA 357
QY 550 GCGTCTGCTGTATCAACGTCACGACGGAAGGCTACCGCTTCCGCTCTGTTTCGATC 609
Db 358 CTTCTCGGGTCAATTTCTGTAACCCGAAACCGGAGTACCGGTTCCCGCTTGTTCCTTT 417
QY 610 TCGTGCGACCCGAACTACAGTTTCAGCATCGAGGGGACAACTCTGACCGTATCGAGGTC 669
Db 418 TCATGCGATCCTAATATTATGTTATTTCTCATGATGGGCATACCATGACTGTTATTGAGGTC 477
QY 670 GACGGTATCAACAGCAGCGCTCTCCTTGTGCACTCTATCCAGATCTTCGCGCGCGCAGGC 729
Db 478 GACGGAGTTAAGCTTCAACCTCTCGTTGTGCACTCGATTCGAGATCTTTCGAGGTCAGCGC 537
QY 730 TACTCCTTTGTTGAATCGAACCAACGTCGGCAACTACTTGGTCCGCGCAACCCG 789

[illegible]

Search completed: December 14, 2002, 05:19:26
Job time : 291 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: December 14, 2002, 06:54:27 ; Search time 70 Seconds
(without alignments)
949.887 Million cell updates/sec

Title: US-09-786-960-2

Perfect score: 2669

Sequence: 1 AIGPVASLVANAPVSPDGF.....VPKAWSDLCPIYDGLSEANQ 499

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2669	100.0	499	21	Trametes versicolor
2	2669	100.0	499	23	Trametes versicolor
3	2656	99.5	499	19	Polyporus pinnatus
4	2656	99.5	499	19	Polyporus pinnatus
5	2656	99.5	519	17	Laccase-LCC2. Pol
6	2238	83.9	499	11	Amino acid sequenc
7	2238	83.9	499	11	Phenol oxidase (PO
8	2238	83.7	499	11	Phenol oxidase (PO
9	2201	82.5	499	19	Polyporus pinnatus
10	2201	82.5	499	19	Polyporus pinnatus

11	2194	82.2	499	19	AAW76296	Polyporus pinnatus
12	2194	82.2	520	17	AAW90721	Laccase-LCC1. Pol
13	2191	82.1	499	19	AAW76297	Polyporus pinnatus
14	2187	81.9	520	23	ABB7510	Trametes versicolor
15	2185	81.9	499	19	AAW76298	Polyporus pinnatus
16	2178	81.6	499	19	AAW76298	Polyporus pinnatus
17	2113	79.2	524	20	AAW92810	T. versicolor lacc
18	1917.5	71.8	527	17	AAW90725	Laccase-LCC5. Pol
19	1842	69.0	511	17	AAW90724	Laccase-LCC4. Pol
20	1772	66.4	512	17	AAW90723	Laccase-LCC3. Pol
21	1772	66.4	518	23	AAU96688	Lentinula edodes p
22	1748.5	65.5	533	21	AAW93952	Amino acid sequenc
23	1748.5	65.5	533	21	AAW93953	Amino acid sequenc
24	1716	64.3	548	13	AAW20735	Laccase enzyme. p
25	1716	64.3	548	19	AAW76309	Phlebia radiata la
26	1704.5	63.9	548	19	AAW60877	Phlebia radiata la
27	1704.5	63.9	517	18	AAW17975	Coprinus cinereus
28	1667.5	62.5	516	18	AAW17974	Coprinus cinereus
29	1598	59.9	518	19	AAW61387	Schizophyllum comm
30	1577.5	59.1	533	23	AAU96689	Lentinula edodes p
31	1533	57.4	539	18	AAW17973	Coprinus cinereus
32	1533	57.4	539	19	AAW76281	Coprinus cinereus
33	1533	57.4	539	19	AAW60874	Coprinus cinereus
34	1505	56.4	539	19	AAW76282	Coprinus cinereus
35	1477.5	55.4	505	23	AAU96690	Lentinula edodes p
36	1431.5	53.6	548	23	AAU96691	Lentinula edodes p
37	1178.5	44.2	529	19	AAW76310	Rhizoctonia solani
38	1178.5	44.2	529	19	AAW60878	Rhizoctonia solani
39	1178.5	44.2	529	21	AAW50728	R. solani laccase
40	1176.5	44.1	529	16	AAW72328	Laccase Rslac3. R
41	1169.5	43.8	529	18	AAW16301	Rhizoctonia solani
42	1000	37.5	599	19	AAW76311	Rhizoctonia solani
43	1000	37.5	599	19	AAW60879	Rhizoctonia solani
44	983	36.8	599	16	AAW72319	Laccase Rslac2 pro
45	930.5	34.9	572	19	AAW76312	Rhizoctonia solani

ALIGNMENTS

RESULT 1
AAW92248
ID AAW92248 standard; Protein; 499 AA.
XX
AC AAW92248;
XX
AC AAW92248;
DT 10-AUG-2000 (first entry)
XX
DE Trametes versicolor laccase.
XX
KW Laccase; transgenic plant; large scale production; paper; pulp;
KW lignin; degradation; biosynthesis.
XX
OS Trametes versicolor.
XX
PN WO200020615-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23256.
XX
PR 05-OCT-1998; 98US-0103031.
XX
(PROD-) PRODIGENE INC.
XX
PI Hood E, Howard J, Jilka J;
XX
DR WPI; 2000-303793/26.
XX
N-PSDB; AAA09191.
XX
Industrial scale laccase production in recombinant corn and maize
plants to produce enzymes for use in the paper industry
XX

Example 1; Page 17-19; 34pp; English.

PS The Trametes versicolor laccase gene can be used to create transgenic
XX plants which produce laccase at levels of about 0.01% or higher of the
CC total soluble protein of the plant. The transgenic plants may be used
CC for the large scale production of laccase enzymes. Laccase is mainly
CC used in the paper and pulp industry for breaking down lignin.
CC Conversely, laccase is also involved in lignin biosynthesis and the
CC formation of lignin polymers. It is therefore useful as a biological
CC adhesive for gluing wood (e.g. in the production of plywood, oriented
CC strand board, particle board and medium density fiberboard). Laccase
CC may also be used for catalyzing the oxidation of compounds such as
CC o,p-diphenols, aminophenols, polyamines and inorganic ions. It is
CC also used as a marker enzyme in enzyme immunoassays, for the oxidation
CC of steroids and the synthesis of vinblastine (a cytostatic compound
CC used in treating malignant diseases).

XX SQ Sequence 499 AA;

Query Match 100.0%; Score 2669; DB 21; Length 499;
Best Local Similarity 100.0%; Pred. No. 7.4e-218;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIGPVASLVANAPVSPDGFRLDRAIVVNGVVPSPPLITGKGRFQLNVVDLTNHSMLKS 60
Db 1 AIGPVASLVANAPVSPDGFRLDRAIVVNGVVPSPPLITGKGRFQLNVVDLTNHSMLKS 60
Qy 61 TSIHWHGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 61 TSIHWHGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Qy 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180
Db 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180
Qy 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Db 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Qy 241 AQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYQGAPVAEPTTTQTTSVIPL 300
Db 241 AQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYQGAPVAEPTTTQTTSVIPL 300
Qy 301 IETNHLPLARMPVPGSPPTGGVDKALNLAFFNCTNFFINNATFTPTVPVLLQILSGAQ 360
Db 301 IETNHLPLARMPVPGSPPTGGVDKALNLAFFNCTNFFINNATFTPTVPVLLQILSGAQ 360
Qy 361 TAQDILLPAGSVYPLPAHSTIETITLPATAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420
Db 361 TAQDILLPAGSVYPLPAHSTIETITLPATAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420
Qy 421 IFRDVVSTGTPAAGDNVTRFQDNPFPWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 421 IFRDVVSTGTPAAGDNVTRFQDNPFPWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 481 PKAWSDLCPYDGLSEANQ 499

RESULT 2
ABB05377

ID ABB05377 standard; Protein; 499 AA.

AC ABB05377;

XX 09-APR-2002 (first entry)

DT Trametes versicolor laccase I protein.

XX Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
KW copper; metal cofactor; plant.

XX

OS Trametes versicolor.

XX PN WO200196543-A2.

XX PD 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US19174.

XX 15-JUN-2000; 2000US-211732P.

XX (PROD-) PRODIGENE INC.

XX (GEMV) GENENCOR INC.

XX Hood E, Howard JA, Bailey M, Van Gastel FJC, Ward M, Wang H;

XX Woodard S;

XX WPI: 2002-090204/12.

XX N-PSDB; ABA92910.

XX Improving recovery of active enzyme e.g. laccase, which requires
PT transitional metal cofactor e.g. copper for activity, from a plant, by
PT introducing plant nucleotide sequences encoding the enzyme and exposing
PT it to cofactor.

XX Example 1; Fig 1A-C; 81pp; English.

XX The present invention describes a method for improving the recovery of
CC an active enzyme from a plant where the enzyme requires a transitional
CC metal cofactor for activity. The method comprises introducing into the
CC plant nucleotide sequences encoding the enzyme and exposing the enzyme
CC to the metal cofactor. The method is useful for improving recovery of
CC an active enzyme which requires a transitional metal cofactor for activity,
CC preferably for improving recovery of active laccase which requires
CC copper for activity. The method can be used for improving recovery of
CC active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires
CC zinc, nickel, cobalt or manganese for activity, where the method further
CC comprises adding bicarbonate ion salt. The present sequence represents
CC the fungal Trametes versicolor laccase I enzyme. Laccases are also called
CC blue copper oxidases and use copper to accept and donate electrons in
CC the oxidation and reduction of substrates.

XX SQ Sequence 499 AA;

Query Match 100.0%; Score 2669; DB 23; Length 499;

Best Local Similarity 100.0%; Pred. No. 7.4e-218;

Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIGPVASLVANAPVSPDGFRLDRAIVVNGVVPSPPLITGKGRFQLNVVDLTNHSMLKS 60

Db 1 AIGPVASLVANAPVSPDGFRLDRAIVVNGVVPSPPLITGKGRFQLNVVDLTNHSMLKS 60

Qy 61 TSIHWHGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120

Db 61 TSIHWHGFFQAGTNWADGPAFVNOCPTASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120

Qy 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180

Db 121 RGPVVYDPKDPHASRYDNDNESTVITLTDWYHTAARLGPFPGLGADATLNLGLRSAST 180

Qy 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240

Db 181 PTAALAVINVQHGKRYRFLYSISCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFA 240

Qy 241 AQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYQGAPVAEPTTTQTTSVIPL 300

Db 241 AQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYQGAPVAEPTTTQTTSVIPL 300

Qy 301 IETNHLPLARMPVPGSPPTGGVDKALNLAFFNCTNFFINNATFTPTVPVLLQILSGAQ 360

Db 301 IETNHLPLARMPVPGSPPTGGVDKALNLAFFNCTNFFINNATFTPTVPVLLQILSGAQ 360

Qy 361 TAQDILLPAGSVYPLPAHSTIETITLPATAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420

Db 361 TAQDILLPAGSVYPLPAHSTIETITLPATAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420

Db 361 TAQDLLPAGSVYPLPAHSTIETTLATAPALGAPHPFLHGHAFVAVRSAGSTTYNNDP 420
QY 421 IFRDVSSTGTGAAGDNVTRFQTDNPGPWFELHCHIDFHLADAGFAIVFAEDVADVKAANPV 480
Db 421 IFRDVSSTGTGAAGDNVTRFQTDNPGPWFELHCHIDFHLADAGFAIVFAEDVADVKAANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 481 PKAWSDLCPYDGLSEANQ 499

RESULT 3
AAW76308
ID AAW76308 standard; protein: 499 AA.
XX
AC AAW76308;
XX
DT 08-JAN-1999 (first entry)
XX
DE Polyporus pinsitus (II) laccase protein.
XX
KW Laccase; variant; oxidation; dye transfer inhibition; bleaching;
KW denim; lignin modification; paper strengthening; phenol polymerisation;
KW hair dye; waste water treatment.
XX
OS Polyporus pinsitus.
PN W09838287-A1.
XX
PD 03-SEP-1998.
XX
PF 23-FEB-1998; 98WO-DK00070.
PR 28-FEB-1997; 97DK-000022.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Svendsen A, Xu F;
XX
DR WPI; 1998-495393/42.
XX
PT New variants of Coprinus and related laccases with increased
PT oxidation potential - or altered pH optimum, or mediator or
PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
PT dye transfer and in bleaching textiles, especially as detergent
PT additive
XX
PS Disclosure; Pages 120-122; 147pp; English.
XX
CC The present sequence represents a laccase protein. The specification
CC describes active laccase variants (see AAW76282, AAW76296-99 and
CC AAW76316-17) having increased oxidation potential, altered pH optimum,
CC altered mediator and/or altered oxygen/hydroxide ion pathway. The
CC laccase variants are used specifically to oxidise substrates, to
CC inhibit dye transfer, and for bleaching textiles, specifically denim.
CC They can also be used for lignin modification, strengthening paper,
CC polymerisation of phenols, dyeing of hair and textiles and waste
CC water treatment.
XX
SQ Sequence 499 AA;

Query Match 99.5%; Score 2656; DB 19; Length 499;
Best Local Similarity 99.4%; Pred. No. 9.4e-217;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AIGPVASLVANAPVSPDGLRDAIVNGVVPSPPLITGKGDRFOLNVVDLTITNHSMLKS 60
Db 1 AIGPVASLVANAPVSPDGLRDAIVNGVVPSPPLITGKGDRFOLNVVDLTITNHSMLKS 60
QY 61 TSIHWHGFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
Db 61 TSIHWHGFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120

QY 121 RGPFFVYDPKDPHASRYDVDNESTVITLTDWYHTAARLGPRPPLGADATLINGLRSAST 180
Db 121 RGPFFVYDPKDPHASRYDVDNESTVITLTDWYHTAARLGPRPPLGADATLINGLRSAST 180
QY 181 PTAALAVINVOHGKRYRFLSVISCDPNYTFSIDGHNITVIEVDGINSOPLLVDSIQIFA 240
Db 181 PTAALAVINVOHGKRYRFLSVISCDPNYTFSIDGHNITVIEVDGINSOPLLVDSIQIFA 240
QY 241 AQRYSEVLNANOTGVNWRANPNFTGTFAGGINSAILRYOGAPVAEPTTTQTTSVIPL 300
Db 241 AQRYSEVLNANOTGVNWRANPNFTGTFAGGINSAILRYOGAPVAEPTTTQTTSVIPL 300
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGFNFFINNATFTPTVPVLLQLLSAQ 360
Db 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFFNGFNFFINNATFTPTVPVLLQLLSAQ 360
QY 361 TAQDLLPAGSVYPLPAHSTIETTLATAPALGAPHPFLHGHAFVAVRSAGSTTYNNDP 420
Db 361 TAQDLLPAGSVYPLPAHSTIETTLATAPALGAPHPFLHGHAFVAVRSAGSTTYNNDP 420
QY 421 IFRDVSSTGTGAAGDNVTRFQTDNPGPWFELHCHIDFHLADAGFAIVFAEDVADVKAANPV 480
Db 421 IFRDVSSTGTGAAGDNVTRFQTDNPGPWFELHCHIDFHLADAGFAIVFAEDVADVKAANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 481 PKAWSDLCPYDGLSEANQ 499

RESULT 4
AAW60876
ID AAW60876 standard; Protein: 499 AA.
XX
AC AAW60876;
XX
DT 09-NOV-1998 (first entry)
XX
DE Polyporus pinsitus (II) laccase.
KW Coprinus laccase-like enzyme; enzyme engineering; enzyme stability;
KW detergent; bleaching.
XX
OS Polyporus pinsitus.
XX
FH Key Location/Qualifiers
FT Misc-difference 107 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe or His) at this position"
FT
FT Misc-difference 116 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT
FT Misc-difference 108 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT
FT Misc-difference 152 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT
FT Misc-difference 57 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe, Val, Ile, Leu or Gln) at this
FT position"
XX
PN W09827198-A1.

XX 25-JUN-1998.
XX
XX 16-DEC-1997; 97WO-DK00571.
XX
XX 08-SEP-1997; 97DK-0001021.
XX 19-DEC-1996; 96DK-0001449.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Cherry JR, Pedersen AH, Rasmussen G, Schneider P;
PI Svendsen A;
XX
XX WPI; 1998-362768/31.
XX
XX New laccase variants with improved stability - having amino acid
PT changes based on Coprinus laccase structure, used for e.g.
PT oxidation, dye transfer inhibition or bleaching
XX
XX Claim 11; 143-145; 168pp; English.
XX
XX This is a laccase enzyme of Polyporus pinsitus. The invention
CC relates to the design of new variants of Coprinus-like laccases
CC (see AA60874-79, AA60925 and AA62501-03); the P. pinsitus laccase
CC (II) shows 73.8% homology to C. cinereus laccase. The modifications
CC are based on the previously unknown three-dimensional structure of
CC C. cinereus laccase. Amino acid residues identified as being
CC important to protein stability are identified and altered to
CC improve stability. The variants are typically obtained by
CC mutagenesis of laccase DNA and expression in a host cell. Variants
CC are preferably modified within 15 (especially 10 or 5) Angstrom
CC of a copper ion in the three-dimensional structure of the laccase.
CC For P. pinsitus (II) laccase variants, preferred substitutions are
CC one or more of W107F/H, Y116F, Y108F, Y152F or M57E/V/L/Q. The
CC stabilised laccase variants can be used in detergent additives, for
CC dye transfer inhibition in detergents, in bleaching of textiles (in
CC particular denim), for lignin modification, paper strengthening,
CC phenol polymerisation, hair dyeing and in waste water treatment.
XX
XX
SQ Sequence 499 AA;
Query Match 99.5%; Score 2656; DB 19; Length 499;
Best Local Similarity 99.4%; Pred. No. 9.4e-217;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AIGPVASLVVANAPVSPDGLRDAIVVNGVVPSPPLTGKGRFQNLNVDTLNHSLKLS 60
DB 1 AIGPVASLVVANAPVSPDGLRDAIVVNGVVPSPPLTGKGRFQNLNVDTLNHSLKLS 60
QY 61 TSIHWGFFOAGTNWAGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 61 TSIHWGFFOAGTNWAGPAFVNOCPITAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
QY 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLNLGHSAST 180
DB 121 RGFVVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLNLGHSAST 180
QY 181 PTAALAVINVQHGKRYFRVLVSTSCDPNTYFSDIGHNLTIVIEDGINSQPLLVDSIQIFA 240
DB 181 PTAALAVINVQHGKRYFRVLVSTSCDPNTYFSDIGHNLTIVIEDGINSQPLLVDSIQIFA 240
QY 241 AQRYSFVLNANQTVGNVWRANFNFGTVGAGGINSAILRYQAGPAEPTTTQTTSTVIPL 300
DB 241 AQRYSFVLNANQTVGNVWRANFNFGTVGAGGINSAILRYQAGPAEPTTTQTTSTVIPL 300
QY 301 IETNLHPLARMPVPGSTPGCGVDKALNLAENFNGTNFFINNATFTPTVPLVLIQLISGAQ 360
DB 301 IETNLHPLARMPVPGSTPGCGVDKALNLAENFNGTNFFINNATFTPTVPLVLIQLISGAQ 360
QY 361 TAODLLPAGSVYPLPAHSTTEITLPTALAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420
DB 361 TAODLLPAGSVYPLPAHSTTEITLPTALAPGAPHPFHLGHAFVAVRSAGSTTYNNDP 420

QY 421 IFRDVYSTGTTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLHDAGFAIVFAEDVADYKAANPV 480
DB 421 IFRDVYSTGTTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLHDAGFAIVFAEDVADYKAANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
DB 481 PKAWSDLCPYDGLSEANQ 499
RESULT 5
AAR90722
ID AAR90722 standard; Protein; 519 AA.
XX
XX AAR90722;
XX
XX 07-APR-1996 (first entry)
XX
XX Laccase-LCC2.
XX
XX Laccase-LCC2; Polyporus pinsitus; Trametes villosa;
KW signal peptide; Aspergillus; cDNA probe; Escherichia coli;
KW plasmid pDSY19; lignin; lignosulphonate; polymerisation; Kraft pulp;
KW depolymerisation; oxidation; hair dye; phenol; aniline; vector;
XX cloning; basidiomycetes.
OS Polyporus pinsitus.
OS Trametes villosa.
FH Key Location/Qualifiers
FT Peptide 1..20 /note= "Signal peptide"
XX
XX WO96000290-A1.
XX 04-JAN-1996.
XX
XX 15-JUN-1995; 95WO-US07536.
XX
XX 15-MAY-1995; 95US-0441147.
XX 24-JUN-1994; 94US-0265534.
XX
XX (NOVO) NOVO NORDISK BIOTECH INC.
XX (NOVO) NOVO-NORDISK AS.
XX
XX Aaslyng DA, Dalboge H, Schneider P, Xu F, Yaver DS;
XX
XX WPI; 1996-068874/07.
XX N-PSDB; AAT15599.
XX
XX DNA constructs for expression of Polyporus laccase enzymes - for use
PT in e.g. lignin manipulation, juice mfr., phenol polymerisation and
PT phenol resin prodn
XX
XX Claim 5; Page 65-67; 137pp; English.
XX
XX The sequence corresponds to laccase-LCC2 (pi 5.95) from Polyporus
CC pinsitus (Trametes villosa). A cDNA probe is obtained by
CC expression in Aspergillus oryzae, and used to screen a P. pinsutus
CC genomic library in Escherichia coli DH5-alpha, giving plasmid
CC pDSY19 (23GEN), with an 4-kb HindIII insert (NRRL B-21266).
CC Screening also results in isolation of genes encoding 4 other
CC laccases produced by P. pinsutus, LCC1 (AAR90721) and LCC3-LCC5
CC (AAR90723-R90725). The laccases may be used to polymerise lignin or
CC lignosulphonates, to depolymerise Kraft pulp, to oxidise dyes or
CC precursors, in hair dye compositions, or to polymerise or oxidise
CC a phenolic or aniline compound. These new laccases are
CC well-expressed in Aspergillus spp. (with vector integration in the
CC genome), in contrast to previous basidiomycete laccases, which give
CC low yields of recombinant enzyme.
XX
XX Sequence 519 AA;
Query Match 99.5%; Score 2656; DB 17; Length 519;

Best Local Similarity 99.4%; Pred. No. le-216;		
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		
Qy	1 AIGPVASLVVANAPVSPDGLDAIVNGVVPSPDLTGKGRFOLNVVDVLTNHSMLKS 60	
Db	21 AIGPVASLVVANAPVSPDGLDAIVNGVVPSPDLTGKGRFOLNVVDVLTNHSMLKS 80	
Qy	61 TSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFVHSHLSTQYCDGL 120	
Db	81 TSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFVHSHLSTQYCDGL 140	
Qy	121 RGFVVDVDPKPHASRYDVDNESVITLTDNYHTAARLGPRFPLGADATLNGLGRSAST 180	
Db	141 RGFVVDVDPKPHASRYDVDNESVITLTDNYHTAARLGPRFPLGADATLNGLGRSAST 200	
Qy	181 PTAALAVINVQHGKRYRFLVSIISCDPNYTFSIDGHNLTVIEVDGINSQPLLVDISIIFA 240	
Db	201 PTAALAVINVQHGKRYRFLVSIISCDPNYTFSIDGHNLTVIEVDGINSQPLLVDISIIFA 260	
Qy	241 AQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTQTTSVPL 300	
Db	261 AQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTQTTSVPL 320	
Qy	301 IETNLHPLARMPVPGSPTPGGVDRKALNLAFFNGTNEFFINNATETPTVPVLLQLLSGAQ 360	
Db	321 IETNLHPLARMPVPGSPTPGGVDRKALNLAFFNGTNEFFINNATETPTVPVLLQLLSGAQ 380	
Qy	361 TAQDLLPAGSVYPLPAHSTIETITPATALAPGAPHPFHLGHAFVAVRSAGSTTYNYNDP 420	
Db	381 TAQDLLPAGSVYPLPAHSTIETITPATALAPGAPHPFHLGHAFVAVRSAGSTTYNYNDP 440	
Qy	421 IFRDVSSTGTTPAAGDNVTIRFQTNPGPWFVLRCHIDFHLDAAGFAIVFAEDVADYKAAAPV 480	
Db	441 IFRDVSSTGTTPAAGDNVTIRFQTNPGPWFVLRCHIDFHLDAAGFAIVFAEDVADYKAAAPV 500	
Qy	481 PRAWSDLCPIYDGLSEANQ 499	
Db	501 PRAWSDLCPIYDGLSEANQ 519	
RESULT 6		
AAR05279		
ID	AAR05279 standard; protein; 499 AA.	
XX	AAR05279;	
XX		
XX	18-AUG-1990 (first entry)	
XX	Amino acid sequence of phenol oxidase (PO).	
DE		
XX	Phenol oxidase (PO); biological pulping; enzyme.	
KW		
XX	JF02005877-A.	
PN		
PD	10-JAN-1990.	
XX		
XX	16-JUN-1988; 88JP-0149103.	
PF		
XX		
PR	16-JUN-1988; 88JP-0149103.	
XX		
XX	(QJIP) QJI PAPER KK.	
XX		
XX	WPI; 1990-053914/08.	
DR	N-PSDB; AAQ03366, AAN93367.	
XX		
XX	Phenol oxidase gene - used for biological pulping, etc.	
PT		
XX	Page 812-813; Fig 2; 14pp; Japanese.	
PS		

CC	It is very pure and it is useful as a biochemical or diagnostic reagent.					
CC	The same sequence is found in JO 2005-876-A.					
xx						
SQ	Sequence	439 AA;				
	Query Match	83.9%; Score 2238; DB 11; Length 499;				
	Best Local Similarity	81.6%; Pred. No. 2.9e-181;				
	Matches 407; Conservative	35; Mismatches 57; Indels 0; Gaps 0;				
Oy	1 AIGPVASIVLVANAPVSPDGLFRLDAIVGVNVPPLITGKKGRFQLNVDTLTNHSMLKS	60				
Db	1 AIGPTADLTISNAEVSPPDFARQAVVNNTTPGLVAGNGDRFLQVLINLTHMLKS	60				
Oy	61 TSIHHWGFQAGTNNWAGPAFVNOCPITASGHSFLYDFHVPDAQTFWYHSHLSYQCDGL	120				
Db	61 TSIHHWGFQGTNNWAGPAFVNOCPISSGHSFLYDFQVPDAQTFWYHSHLSYQCDGL	120				
Oy	121 RGPFFVVDKDPHASRYDVDNESVTILTDMYHTAARLGPRFLGADATLINGLRSA	180				
Db	121 RGPFFVVDNDPHASLDYDVNDMDTVIINLAWMYHTAAKLGPALGADATLINGLRSP	180				
Oy	181 PTAALAVINVQHGRKRYRFLVSLISCDPNYTFSDIGHNLTVIEVDGINSQLLVDSIQIFA	240				
Db	181 TAADLAVINTVKGRYRFLVSLSCDPNHFTSIDGHDLTIEVDSINSQPLVDSIQIFA	240				
Oy	241 AQRSFVLNANOQTGNVTWRANPNEFTVGFGAGINSAILRYOGAPVAEPPTQTTSVIPL	300				
Db	241 AQRSFVLNADOQVGNVIRANPNFNMGVFGAGINSAILRYDGADPEPTTQTTPKPL	300				
Oy	301 IETNLHLPMRPVPGSPTPGGVDKALNALNFNCTNFFINNATPTPTVPVLLQILSGAQ	360				
Db	301 NEVDLHLPLATAWPVPGSPVAGGVDTAINMAFNFNCTNFFINGASFVPTVPVLLQISSAQ	360				
Oy	361 TAODLLPAGSVYPPLPAHSTTEITLPATALAPGAPHFHLHGHAFAVVRSGSTTYNYNDP	420				
Db	361 NAQDLLPGSVYSLPSNADIESPATAAAPGAPHPFHLHGHAFAVVRSGSTVINYNDP	420				
Oy	421 IFRDWSTGTGAAGDNVTIRFOTDPCGWFLHCHIDFHLDAGFAIVFAEDVADVKAANPV	480				
Db	421 IFRDWSTGTGAAGDNVTIRFOTDPCGWFLHCHIDFHLEAGFAVVFAEDIPDVASANPV	480				
Oy	481 PKAWSDLCLPYDGLSEANQ	499				
Db	481 PQAWSDLCLPYDALDVNDQ	499				
RESULT	7					
AAR07068	ID	AAR07068 standard; protein; 499 AA.				
XX	AC	AAR07068;				
XX	DT	03-FEB-1991 (first entry)				
XX	DE	Phenol oxidase (PO) gene product.				
XX	KW	Paper pulping.				
XX	FN	JF02027986-A.				
XX	PD	30-JAN-1990.				
XX	PF	15-JUL-1988; 88JP-0175236.				
XX	PR	15-JUL-1988; 88JP-0175236.				
XX	PA	(OJIP) OJI FAPER KK.				
XX	DR	WPI; 1990-323326/43.				
XX	PT	N-PSDB; AAQ03571.				
XX	New phenol oxidase gene - has DNA encoding specified sequence of 499 aminoacid(s)					

```
XX Claim 1; Page 559; 15pp; Japanese.
XX PO is useful in biological paper pulping and bleaching.
XX
XX Sequence 499 AA;
XX
Query Match 83.9%; Score 2238; DB 11; Length 499;
Best Local Similarity 81.6%; Pred. No. 2.9e-181;
Matches 407; Conservative 35; Mismatches 57; Indels 0; Gaps 0;
QY 1 AIGPVASLVANAPVSPDGLRDAIVVGVVSPSLITGKGRFQNLNVDTLNNHMLKS 60
DB 1 AIGPTADLTISNAEVSDFGARQAVVNVNTPGLVAGNKGDRFQNLNLTNHTMLKS 60
QY 61 TSHHGHFFQAGTNWADGPAFVNOCPITASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 61 TSHHGHFFQAGTNWADGPAFVNOCPITSSGHSLYDFQVDPDQAGTFWYHSHLSTQYCDGL 120
QY 121 RGFVVYDPRKDPHASRYDVNDNESTVITLTQWYHTAARLGRFPLGADATLNLGRSAST 180
DB 121 RGFVVYDPRNDPHASLYDVNDNDTVINLADWYHTAAKLGPAFPLGADATLNLGRSPST 180
QY 181 PTAALAVINVQHGKRYRFRVLSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSIQIFA 240
DB 181 TAADLAVINVTKGRYRFRVLSLSCDPNHTFSIDGHDLTIEVDSINSQPLVVDSTQIFA 240
QY 241 AQRYSFVLNANQTVGNVWRANFNGVGFAGGINSAILRYOGAPVAEPTTTQTTTSVIPL 300
DB 241 AQRYSFVLNADQDVGNVWRANFNGVGFAGGINSAILRYDGADPVEPTTTQTTTKPL 300
QY 301 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTNEFFINNATFTPTVPVLLQILSGAQ 360
DB 301 NEVDLHPLATMAYPGSPVAGGVDTAINWAFNENGTNEFFINGASFVPTVPVLLQILSGAQ 360
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLHGHAFVAVRSAGSTTYNDP 420
DB 361 NAQDLLPSGSVYSLPSNADIEISFPATAAAPPAPHPHLLHGHAFVAVRSAGSTVYNDP 420
QY 421 IFRDVVSTGTPAAGDNVTIRFOTDNPWFLLHCHIDPHLDAGFAIVFAEDVADVKAANPV 480
DB 421 IFRDVVSTGTPAAGDNVTIRFOTDNPWFLLHCHIDPHLDAGFAIVFAEDIPDVASANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
DB 481 PKAWSDLCPYDALDVNDQ 499
RESULT 8
AAR07069
ID AAR07069 standard; protein; 499 AA.
AC AAR07069;
XX
XX 03-FEB-1991 (first entry)
XX
XX Phenol oxidase (PO) gene product.
XX
XX Paper pulping.
XX
XX JF02027986-A.
XX
XX 30-JAN-1990.
XX
XX 15-JUL-1988; 88JP-0175236.
XX
XX 15-JUL-1988; 88JP-0175236.
XX
XX (OJIP ) OJI PAPER KK.
XX
XX WPI; 1990-323326/43.
XX
XX N-PSDB; AAQ03572.
XX
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```
PT New phenol oxidase gene - has DNA encoding specified sequence of
PT 499 aminoacid(s)
XX
XX Claim 1; Page 559; 15pp; Japanese.
XX
XX PO is useful in biological paper pulping and bleaching.
XX
XX Sequence 499 AA;
XX
Query Match 83.7%; Score 2233; DB 11; Length 499;
Best Local Similarity 81.4%; Pred. No. 7.6e-181;
Matches 406; Conservative 35; Mismatches 58; Indels 0; Gaps 0;
QY 1 AIGPVASLVANAPVSPDGLRDAIVVGVVSPSLITGKGRFQNLNVDTLNNHMLKS 60
DB 1 AIGPTADLTISNAEVSDFGARQAVVNVNTPGLVAGNKGDRFQNLNLTNHTMLKS 60
QY 61 TSHHGHFFQAGTNWADGPAFVNOCPITASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
DB 61 TSHHGHFFQAGTNWADGPAFVNOCPITSSGHSLYDFQVDPDQAGTFWYHSHLSTQYCDGL 120
QY 121 RGFVVYDPRKDPHASRYDVNDNESTVITLTQWYHTAARLGRFPLGADATLNLGRSAST 180
DB 121 RGFVVYDPRNDPHASLYDVNDNDTVINLADWYHTAAKLGPAFPLGADATLNLGRSPST 180
QY 181 PTAALAVINVQHGKRYRFRVLSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSIQIFA 240
DB 181 TAADLAVINVTKGRYRFRVLSLSCDPNHTFSIDGHDLTIEVDSINSQPLVVDSTQIFA 240
QY 241 AQRYSFVLNANQTVGNVWRANFNGVGFAGGINSAILRYOGAPVAEPTTTQTTTSVIPL 300
DB 241 AQRYSFVLNADQDVGNVWRANFNGVGFAGGINSAILRYDGADPVEPTTTQTTTKPL 300
QY 301 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTNEFFINNATFTPTVPVLLQILSGAQ 360
DB 301 NEVDLHPLATMAYPGSPVAGGVDTAINWAFNENGTNEFFINGASFVPTVPVLLQILSGAQ 360
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLHGHAFVAVRSAGSTTYNDP 420
DB 361 NAQDLLPSGSVYSLPSNADIEISFPATAAAPPAPHPHLLHGHAFVAVRSAGSTVYNDP 420
QY 421 IFRDVVSTGTPAAGDNVTIRFOTDNPWFLLHCHIDPHLDAGFAIVFAEDVADVKAANPV 480
DB 421 IFRDVVSTGTPAAGDNVTIRFOTDNPWFLLHCHIDPHLDAGFAIVFAEDIPDVASANPV 480
QY 481 PKAWSDLCPYDGLSEANQ 499
DB 481 PKAWSDLCPYDALDVNDQ 499
RESULT 9
AAW76295
ID AAW76295 standard; protein; 499 AA.
XX
XX AAW76295;
XX
XX 08-JAN-1999 (first entry)
XX
XX Polyporus pinsitus (I) laccase protein.
XX
XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;
XX denim; lignin modification; paper strengthening; phenol polymerisation;
XX hair dye; waste water treatment.
XX
XX Polyporus pinsitus.
XX
XX WO9838287-A1.
XX
XX 03-SEP-1998.
XX
XX 23-FEB-1998; 98WO-DK00070.
XX
XX 28-FEB-1997; 97DK-0000222.
XX
```


XX PA (NOVO) NOVO-NORDISK AS.
XX PI Svendsen A, Xu F;
XX WPI; 1998-495393/42.
XX New variants of Coprinus and related laccases with increased
PT oxidation potential - or altered pH optimum, or mediator or
PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
PT dye transfer and in bleaching textiles, especially as detergent
PT additive
XX Disclosure; Pages 119-120; 147pp; English.
XX The present sequence represents a laccase protein. The specification
CC describes active laccase variants (see AAW76282, AAW76296-99 and
CC AAW76316-17) having increased oxidation potential, altered pH optimum,
CC altered mediator and/or altered oxygen/hydroxide ion pathway. The
CC laccase variants are used specifically to oxidise substrates, to
CC inhibit dye transfer, and for bleaching textiles, specifically denim.
CC They can also be used for lignin modification, strengthening paper,
CC polymerisation of phenols, dyeing of hair and textiles and waste
XX water treatment.
XX SQ Sequence 499 AA;
Query Match 82.5%; Score 2201; DB 19; Length 499;
Best Local Similarity 80.1%; Pred. No. 3.9e-178;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
QY 2 IGVASLVANAPVSPDGLRDAIVVNGVYVPSPLITKGGDRFQLNVDTLNHSMKST 61
DB 2 IGVADLTITNAASPDSGRQAVVNGTGPCPLITGNMGDRFQLNVIDLNHTMLKST 61
QY 62 SHHWGFFOAGTNGADGAFVNOCTIASHCSFLYDFHPDQAGTFWYHSLSTQYCDGLR 121
DB 62 SHHWGFFOAGTNGADGAFVNOCTIASHCSFLYDFHPDQAGTFWYHSLSTQYCDGLR 121
QY 122 GPFVYDPRKPHASRYDVNDNESTVITLTDTWYHTAARLGRPFPLGADATLINGLRSASTP 181
DB 122 GPFVYDPRNDPAADLYDVNDNDTIVITLVDMYHVAALGPAPFLGADATLINGKRSPTT 181
QY 182 TAAIAVINQHKRFRRLVSLSCDPNTFTSIDGHNLTAVIEVDGINSOPLLVDSIOIFAA 241
DB 182 TADLSVISVTPGKRYRFRRLVSLSCDPNTFTSIDGHNMTIETDSINTAPLVVDSIQIFAA 241
QY 242 QRYSFVLNANQTVGNVWRANFNFTGVGFAGGINSAILRYOGAPVAEPTTOTTSTVPLI 301
DB 242 QRYSFVLEANQAVDNYWIRANFNFTGVGFAGGINSAILRYDGAAVEPTTOTTSTAPLN 301
QY 302 ETNLHPLARMPVPGSFTPGGVDRKALNLAFFNFTGNTFFINNAFTTPTTPVLLQLILSGAQT 361
DB 302 EYNLHPLVTTAVPGSPVAGGVDLAINMAFNFTGNTFFINNGASFTPTTPVLLQLIISGAQN 361
QY 362 AODLLPAGSVPLPAHSITETITLPATAPAGPHFHLGHAFVAVRSAGSTTYNYNDPI 421
DB 362 AODLLPAGSVPLPAHSITETITLPATAPAGPHFHLGHAFVAVRSAGSTTYNYNDPI 421
QY 422 FRDVTSTGTPAAGDNVITRFQDNGPWFHLCHIDHFDAGFAIVFAEDVADVKAANPVP 481
DB 422 FRDVTSTGTPAAGDNVITRFQDNGPWFHLCHIDHFDAGFAIVFAEDVADVKAANPVP 481
QY 482 KAWSDLCPYDGLSEANQ 499
DB 482 QAWSDLCPYDALDPSDQ 499

RESULT 10
AAW60875
ID AAW60875 standard; Protein: 499 AA.
XX
AC AAW60875;

XX DT 09-NOV-1998 (first entry)
XX DE Polyporus pinsitus (I) laccase.
XX KW Coprinus laccase-like enzyme; enzyme engineering; enzyme stability;
XX KW detergent; bleaching.
XX OS Polyporus pinsitus.
XX FH Key Location/Qualifiers
FT Misc-difference 107 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Met, Gly, Ser, Thr, Cys, Tyr, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe or His) at this position"
FT Misc-difference 116 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT Misc-difference 108 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT Misc-difference 152 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Met, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe) at this position"
FT Misc-difference 57 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe, Val, Ile, Leu or Gln) at this
FT position"
FT Misc-difference 328 /note= "variant may have Ala, Val, Leu, Ile, Pro,
FT Phe, Trp, Gly, Ser, Thr, Cys, Tyr, Asn,
FT Gln, Asp, Glu, Lys, Arg or His (preferably
FT Phe, Val, Ile, Leu or Gln) at this
FT position"
XX WO9827198-A1.
XX 25-JUN-1998.
XX 16-DEC-1997; 97WO-DK00571.
XX 08-SEP-1997; 97DK-0001021.
XX 19-DEC-1996; 96DK-0001449.
XX (NOVO) NOVO-NORDISK AS.
XX Cherry JR, Federsen AH, Rasmussen G, Schneider P;
XX Svendsen A;
XX WPI; 1998-362768/31.
XX New laccase variants with improved stability - having amino acid
PT changes based on Coprinus laccase structure, used for e.g.
PT oxidation, dye transfer inhibition or bleaching
XX Claim 10; 142-143; 168pp; English.
XX This is a laccase enzyme of Polyporus pinsitus. The invention
CC relates to the design of new variants of Coprinus-like laccases
CC (see AAW60874-79, AAW60925 and AAW62501-03); the P. pinsitus laccase (I)
CC shows 74.4% homology to C. cinereus laccase. The modifications are
CC based on the previously unknown three-dimensional structure of
CC C. cinereus laccase. Amino acid residues identified as being
CC important to protein stability are identified and altered to

PD 03-SEP-1998.
XX
PF 23-FEB-1998; 98WO-DK00070.
XX
PR 28-FEB-1997; 97DK-0000222.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Svendsen A, Xu F;
XX
XX WPI; 1998-495393/42.
DR
XX New variants of Coprinus and related laccases with increased
PT oxidation potential - or altered pH optimum, or mediator or
PT oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
PT dye transfer and in bleaching textiles, especially as detergent
PT additive
XX
XX Claim 12; Page -: 147pp; English.
XX
CC The present sequence represents a mutant laccase protein. The
CC specification describes active laccase variants (see AAW76282,
CC AAW76296-99 and AAW76316-17) having increased oxidation potential,
CC altered pH optimum, altered mediator and/or altered oxygen/hydroxide
CC ion pathway. The laccase variants are used specifically to oxidise
CC substrates, to inhibit dye transfer, and for bleaching textiles,
CC specifically denim. They can also be used for lignin modification,
CC strengthening paper, polymerisation of phenols, dyeing of hair and
CC textiles and waste water treatment.
CC note: the present sequence does not appear in the specification; it was
CC constructed using information provided.
XX
SQ Sequence 499 AA;
Query Match 82.1%; Score 2191; DB 19; Length 499;
Best Local Similarity 79.9%; Pred. No. 2.8e-177;
Matches 398; Conservative 34; Mismatches 66; Indels 0; Gaps 0;
QY 2 IGPVASLVANAVSPDGLRDAIVVGVVPSPLITGKGRFQNLNVDTLTNHSMLKST 61
DB 2 IGPVADLTITNAAVSPDGFSGRQAVVNGTGPGLITGNMGDRFQNLNVDTLTNHSMLKST 61
QY 62 SIHHGFFQAGTNWADGPAFVNCPTASGHSFLYDFHVPDQAGTFWYHSHLSYQCDGLR 121
DB 62 SIHHGFFQAGTNWADGPAFVNCPTASGHSFLYDFHVPDQAGTFWYHSHLSYQCDGLR 121
QY 122 GPVVYDPRDPRASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLINGLGRSASTP 181
DB 122 GPVVYDPRDPRADLYDVNDNDTIVITLDWYHVAALGPAPPLGADATLINGKRSFSTT 181
QY 182 TAALAVINVOHGKRYRFLRVLSISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFAA 241
DB 182 TADLSVISVTPGKRYRFLRVLSISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFAA 241
QY 242 QRYSFVLNANQTVGNVWRANPNFGVGFAGGINSAILRYOGAPVAEPTTQTTSVIPLI 301
DB 242 QRYSFVLEAQAQVNDWIRANPNFGVGFAGGINSAILRYOGAPVAEPTTQTTSVIPLI 301
QY 302 ETMLHPLARMPVPGSPTPGCGDKALNLFNFGTNEFFINNAFTPTPTVPVLLQILSGAQT 361
DB 302 EVNLHPLVITAVPGSPVAGGVDLAINMAFNFGTNEFFINNGASFTPTPTVPVLLQILSGAQN 361
QY 362 AQDLLPAGSVYPLPAHSTIEITLPAALAPGAPPHLHGAFVAVRSAGSTTYNDPI 421
DB 362 AQDLLPAGSVYPLSPNADIEISPPATAAAGAPPHLHGAFVAVRSAGSTTYNDPI 421
QY 422 FRDVVSTGTPAAGDNYTIRFDTNPGFWLHCHIDPHLDAFAIVEADVAKANVPV 481
DB 422 FRDVVSTGTPAAGDNYTIRFDTNPGFWLHCHIDPHLDAFAIVEADVAKANVPV 481
QY 482 KAWSDLCLPTVDGLSEANO 499
DB 482 QAWSDLCLPTVDALPSDQ 499

RESULT 14
ABB77510
ID ABB77510 standard; Protein; 520 AA.
XX
AC ABB77510;
XX
DT 23-AUG-2002 (first entry)
XX
DE Trametes versicolor Laccase III SEQ ID NO 26.
XX
KW Fungi; Thal; Ctal; copper-dependent secreted protein; copper; laccase;
KW Trametes ATRX1 homologue; copper transporting ATPase; enzyme.
XX
OS Trametes versicolor.
XX
PN DE10046932-Al.
XX
PD 16-MAY-2002.
XX
PF 21-SEP-2000; 2000DE-1046932.
XX
PR 21-SEP-2000; 2000DE-1046932.
XX
PA (CONE) CONSORTIUM ELEKTROCHEM IND GMBH.
XX
PI Marbach-Ringhandt K, Pfaller R, Uldschmid A;
XX
DR WPI; 2002-445163/48.
DR N-PSDB; ABL60268.
XX
PT Expression system for increased production of copper-dependent enzymes,
PT particularly laccase, includes the gene for a copper homeostasis
PT protein
XX
PS Disclosure; Page 48-50; 58pp; German.
XX
CC The invention relates to an expression system (A) that provides increased
CC expression of copper-dependent secreted proteins (I) in eukaryotic cells
CC comprises a gene (II) that encodes (I) and at least one cooper
CC homeostasis gene (III). (A) is used to express enzymes, especially
CC laccase, that require copper as co-factor. (III) transports copper to the
CC secretory pathway so its overexpression leads to increased yields of (I).
CC The present sequence is that of the trametes versicolor Laccase III
CC protein of the invention.
XX
SQ Sequence 520 AA;
Query Match 81.9%; Score 2187; DB 23; Length 520;
Best Local Similarity 79.7%; Pred. No. 6.5e-177;
Matches 397; Conservative 36; Mismatches 65; Indels 0; Gaps 0;
QY 2 IGPVASLVANAVSPDGLRDAIVVGVVPSPLITGKGRFQNLNVDTLTNHSMLKST 61
DB 23 IGPVADLTITNAAVSPDGFSGRQAVVNGTGPGLITGNMGDRFQNLNVDTLTNHSMLKST 82
QY 62 SIHHGFFQAGTNWADGPAFVNCPTASGHSFLYDFHVPDQAGTFWYHSHLSYQCDGLR 121
DB 83 SIHHGFFQAGTNWADGPAFVNCPTASGHSFLYDFHVPDQAGTFWYHSHLSYQCDGLR 142
QY 122 GPVVYDPRDPRASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLINGLGRSASTP 181
DB 143 GPVVYDPRDPRADLYDVNDNDTIVITLDWYHVAALGPAPPLGADATLINGKRSFSTT 202
QY 182 TAALAVINVOHGKRYRFLRVLSISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFAA 241
DB 203 TADLTVISVTPGKRYRFLRVLSISCDPNYTFSDIGHNLTVEVDGINSQPLLVDSIQIFAA 262
QY 242 QRYSFVLNANQTVGNVWRANPNFGVGFAGGINSAILRYOGAPVAEPTTQTTSVIPLI 301
DB 263 QRYSFVLEAQAQVNDWIRANPNFGVGFAGGINSAILRYOGAPVAEPTTQTTSVIPLI 322

QY 302 ETNLHPLARMPVPGSTPGGVKALNLAFFNGTFFINNAFTPTPTVLLQILSGAQT 361
Db 323 EVNLHPLVATVPVPGSVAGVDLAINMAFNCTNFFINGASFTPTPTVLLQILSGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATAPGAPHPHLLGHAFVAVRSAGSTTYNDPI 421
Db 383 AQDLLPAGSVYSLPSNADIEISFPATAAAGAPHPHLLGHAFVAVRSAGSTTYNDPI 442
QY 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWFLLCHIDFHLDAFAIVFAEDVADVKAANPVP 481
Db 443 FRDVTSTGTPAAGDNVTIRFRTDNPGPWFLLCHIDFHLDAFAIVFAEDIPDVASANPVP 502
QY 482 KAWSDLCPYDGLSEANQ 499
Db 503 QAWSDLCPYDALDPSDQ 520

RESULT 15

AAW76299

ID AAW76299 standard; protein; 499 AA.

XX AC

AAW76299;

XX 08-JAN-1999 (first entry)

DE Polyporus pinsitus (f) laccase variant protein.

XX Laccase; variant; oxidation; dye transfer inhibition; bleaching;
KW denim; lignin modification; paper strengthening; phenol polymerisation;
KW hair dye; waste water treatment.

XX Synthetic.

OS Polyporus pinsitus.

XX Key

FH Location/Qualifiers

FT Misc-difference 80

FT /label= A80X

FT /note= "X is optionally Asp or Glu"

FT Misc-difference 81

FT /label= F81A

FT /note= "X is optionally Asp or Glu"

FT Misc-difference 112

FT /label= L112X

FT /note= "X is optionally Asp or Glu"

XX W09838287-A1.

XX 03-SEP-1998.

XX 23-FEB-1998; 98WO-DK00070.

XX 28-FEB-1997; 97DK-0000222.

XX (NOVO) NOVO-NORDISK AS.

XX Svendsen A, Xu F;

XX WPI; 1998-495393/42.

DR New variants of Coprinus and related laccases with increased
XX oxidation potential - or altered pH optimum, or mediator or
XX oxygen-hydroxide ion pathways, useful for oxidation, for inhibiting
XX dye transfer and in bleaching textiles, especially as detergent
XX additive

PS Claim 14; Page -: 147pp; English.

XX The present sequence represents a mutant laccase protein. The
XX specification describes active laccase variants (see AAW76282,
XX AAW76296-99 and AAW76316-17) having increased oxidation potential,
XX altered pH optimum, altered mediator and/or altered oxygen/hydroxide
XX ion pathway. The laccase variants are used specifically to oxidise
XX substrates, to inhibit dye transfer, and for bleaching textiles,

CC specifically denim. They can also be used for lignin modification,
CC strengthening paper, polymerisation of phenols, dyeing of hair and
CC textiles and waste water treatment.
CC note: the present sequence does not appear in the specification; it was
CC constructed using information provided.

CC note: residue 260 is defined as Asn in the claims; however residue 260
XX of the wild type protein (AAW76295) is Arg"

SQ Sequence 499 AA;

Query Match 81.9%; Score 2185; DB 19; Length 499;

Best Local Similarity 79.5%; Pred. No. 9e-177;

Matches 396; Conservative 35; Mismatches 67; Indels 0; Gaps 0;

QY 2 IGPVASLVANAPVSPDGLRDAIVVGVVPSPLITGKGGDFQLNVVDLTNHSMLKST 61

Db 2 IGPVADLAFITNAAVSPDGFSAQVAVVNGTGPGLITGNNGDRFQLNVIDNLNHTMLKST 61

QY 62 SIHWHGFTQAGTNWADGPAFVNOCPIASGHSELYDFHVPDQAGTFWYHSHLSLSTQYCDGLR 121

Db 62 SIHWHGFTQAGTNWADGPAFVNOCPIASGHSELYDFHVPDQAGTFWYHSHLSLSTQYCDGLR 121

QY 122 GPFVYDPAKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLNGLRASSTP 181

Db 122 GPFVYDPAKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLNGLRASSTP 181

QY 182 TAALAVIRHVGKRYRFLVSVISCDPNYTFSIDGHNLTVIEVDGINSOPLLVDSIOIFAA 241

Db 182 TAALAVIRHVGKRYRFLVSVISCDPNYTFSIDGHNLTVIEVDGINSOPLLVDSIOIFAA 241

QY 242 QRYSEVLHANQTVGNVVRANPNFTGVPAGGINSAILRYOGAPVAEPTTTTTSVIPLI 301

Db 242 QRYSEVLHANQTVGNVVRANPNFTGVPAGGINSAILRYOGAPVAEPTTTTTSVIPLI 301

QY 302 ETNLHPLARMPVPGSTPGGVKALNLAFFNGTFFINNAFTPTPTVLLQILSGAQT 361

Db 302 ETNLHPLARMPVPGSTPGGVKALNLAFFNGTFFINNAFTPTPTVLLQILSGAQT 361

QY 362 AQDLLPAGSVYPLPAHSTIEITLPATAPGAPHPHLLGHAFVAVRSAGSTTYNDPI 421

Db 362 AQDLLPAGSVYPLPAHSTIEITLPATAPGAPHPHLLGHAFVAVRSAGSTTYNDPI 421

QY 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWFLLCHIDFHLDAFAIVFAEDVADVKAANPVP 481

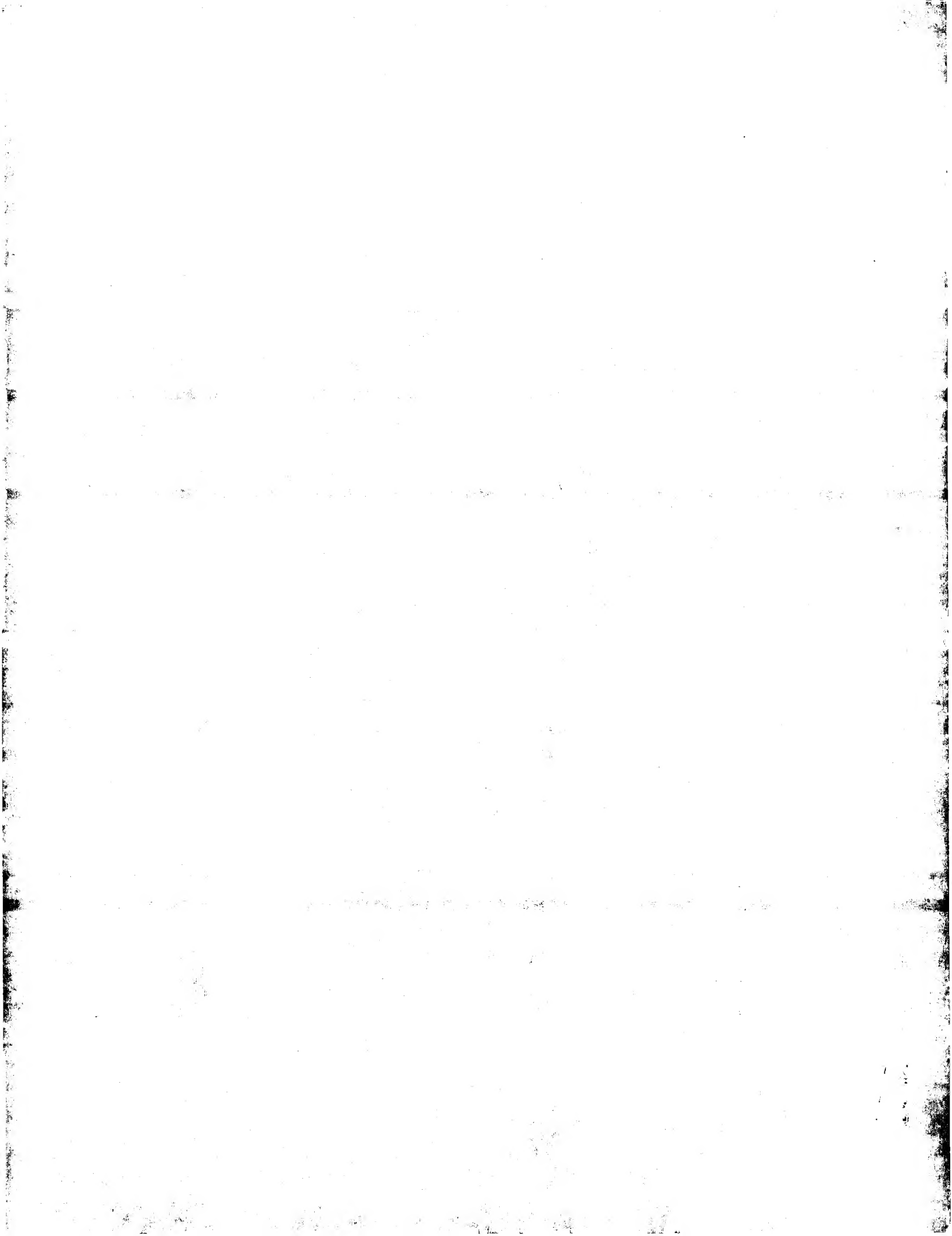
Db 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWFLLCHIDFHLDAFAIVFAEDVADVKAANPVP 481

QY 482 KAWSDLCPYDGLSEANQ 499

Db 482 KAWSDLCPYDGLSEANQ 499

Search completed: December 14, 2002, 08:25:24

Job time : 74 secs



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OM protein - protein search, using sw model

Run on: December 14, 2002, 07:47:02 ; Search time 84 Seconds
 (without alignments)
 1224.018 Million cell updates/sec

Title: US-09-786-960-2
 Perfect score: 2669
 Sequence: 1 AIGPVASIVVANAPVSPDGF.....VPKAWSDLCPIYDGLSEANQ 499

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_21.*
 1: sp_archaea.*
 2: sp_bacteria.*
 3: sp_fungi.*
 4: sp_human.*
 5: sp_invertebrate.*
 6: sp_mammal.*
 7: sp_mhc.*
 8: sp_organelle.*
 9: sp_phase.*
 10: sp_plant.*
 11: sp_rhodent.*
 12: sp_virus.*
 13: sp_vertebrate.*
 14: sp_unclassified.*
 15: sp_kvirus.*
 16: sp_bacteriap.*
 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2599	97.4	519	3 Q96UK8	Q96UK8 trаметes ve
2	2343.5	87.8	519	3 Q13420	Q13420 basidiomyce
3	2195	82.2	520	3 Q96UT7	Q96UT7 trаметes ve
4	2194	82.2	520	3 Q13448	Q13448 coriolus ve
5	2194	82.2	520	3 Q8TG94	Q8TG94 trаметes pu
6	2187	81.9	520	3 Q8TFM1	Q8TFM1 trаметes ve
7	2186	81.9	520	3 Q13421	Q13421 basidiomyce
8	2176	81.5	520	3 Q94222	Q94222 trаметes ve
9	2145	80.4	518	3 Q96TR6	Q96TR6 pycnopus
10	2143	80.3	518	3 Q96VA5	Q96VA5 pycnopus
11	2140	80.2	518	3 Q59896	Q59896 pycnopus
12	2138	80.1	518	3 Q9UVQ2	Q9UVQ2 pycnopus
13	2137	80.1	524	3 Q13422	Q13422 basidiomyce
14	2125	79.6	518	3 Q9HDS9	Q9HDS9 polyporus c
15	2107.5	79.0	521	5 Q61263	Q61263 trachyderma
16	2102.5	78.8	521	3 Q9UVU8	Q9UVU8 pycnopus

ALIGNMENTS

RESULT 1

Q96UK8 PRELIMINARY; PRT: 519 AA.

AC Q96UK8;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Laccase 1 (EC 1.10.3.2).
 GN LAC1.
 OS Trametes versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Trametes.
 OX NCBI_TaxID=5325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CUI;
 RA McClean K.H., O'Brien M.M., Dobson A.D.W.;
 RT "Trametes versicolor laccase (lac1) mRNA sequence.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AY049725; AAL00887.1; -;
 DR InterPro; IPR001117; Cu-oxidase.
 DR Pfam; PF00394; Cu-oxidase; 3.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 519 AA; 55998 MW; 8C9C6934DEAE3E0A CRC64;

Query Match 97.4%; Score 2599; DB 3; Length 519;
 Best Local Similarity 97.4%; Pred. No. 2.9e-177;
 Matches 486; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 AIGPVASIVVANAPVSPDGF...AIVVNGVPSPLITGKKGDRFQLNVVDTLTNHSMLKS 60
 DB 21 AIGPVASIVVANAPVSPDGF...AIVVNGVPSPLITGKKGDRFQLNVVDTLTNHSMLKS 80
 QY 61 TSIHHGHFFQAGTNWADGPAFVNOCPAGSHGFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
 DB 81 TSIHHGHFFQAGTNWADGPAFVNOCPAGSHGFLYDFHVPDQAGTFWYHSHLSTQYCDGL 140
 QY 121 RGFVVYDPKPHASRYDVNDNESTVITLTDWYHTAARLGPFRPLGADATLINGLRASST 180

```
Db 141 RGFVYVDPKPHASRYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 200
|||||
QY 181 PTAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSIQIFA 240
|||||
Db 201 PTAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSIQIFA 260
|||||
QY 241 AQRYSFVLNANOTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTTQTSVPL 300
|||||
Db 261 AQRYSFVLNANOTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTTQTSVPL 320
|||||
QY 301 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTPVLLQLILSGAQ 360
|||||
Db 321 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTPVLLQLILSGAQ 380
|||||
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLGHAFVAVRSAGSTTYNYNDP 420
|||||
Db 381 TAQELLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLGHAFVAVRSAGSTTYNYNDP 440
|||||
QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 480
|||||
Db 441 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLEAGFAIYFAEDVADVKAANPV 500
|||||
QY 481 PKAWSDLCPYDGLSEANQ 499
|||||
Db 501 PKAWSDLCPYDGLSEADQ 519
|||||

RESULT 2
O13420 PRELIMINARY; PRT; 519 AA.
ID O13420
AC O13420
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Phenoloxidase (EC 1.10.3.2).
GN POX1.
OS basidiomycete CECT 20197.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Polyporaceae.
OX NCBI_TaxID=51095;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT N.197;
RX MEDLINE=97355933; PubMed=9212414;
RA Mansur M., Suarez T., Fernandez-Larrea J.B., Brizuela M.A.,
RA Gonzalez A.E.;
RT "Identification of a laccase gene family in the new lignin-degrading
RL Appl. Environ. Microbiol. 63:2637-2646(1997).
RL EMBL; U65399; AAB63443.1; -.
DR HSSP; P37064; LAOZ.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase.
SQ SEQUENCE 519 AA; 55665 MW; CD226C498770DDE4 CRC64;

Query Match 87.8%; Score 2343.5; DB 3; Length 519;
Best Local Similarity 86.5%; Pred. No. 4.8e-159;
Matches 431; Conservative 25; Mismatches 41; Indels 1; Gaps 1;

QY 1 AIGPVASLVANAPVSPDGLRDAIVNGVVPSPPLITGKGRFQNLNVVDLTNHSMLKS 60
|||||
Db 22 AVGE-ADLTITNAVYAPDGSFSDRAIVVNGVVPSPPLITGKGRFQNLNVVDLTNHSMLKS 80
|||||
QY 61 TSIHHGFFOAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGFWYHSHLSTQYCDGL 120
|||||
Db 81 TSIHHGFFOAGTNWADGPAFVNCQPISTGTHAFLYDFHVPDQAGFWYHSHLSTQYCDGL 140
|||||
QY 121 RGFVYVDPKPHASRYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 180
|||||
Db 141 RGFVYVDPKPHASRYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 200
|||||
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QY 181 PTAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSIQIFA 240
|||||
Db 201 PTAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSIQIFA 260
|||||
QY 241 AQRYSFVLNANOTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTTQTSVPL 300
|||||
Db 261 AQRYSFVLNANOTVGNWVRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTTQTSVPL 320
|||||
QY 301 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTPVLLQLILSGAQ 360
|||||
Db 321 IETNLHPLARMPVPGSPTPGGVKALNLAENFNGTFFINNATFTPTPVLLQLILSGAQ 380
|||||
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLGHAFVAVRSAGSTTYNYNDP 420
|||||
Db 381 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPHLLGHAFVAVRSAGSTTYNYNDP 440
|||||
QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLDAGFAIYFAEDVADVKAANPV 480
|||||
Db 441 IFRDVVSTGTPAAGDNVTIRFQTDNPGWFLHCHIDPHLEAGFAIYFAEDVADVKAANPV 500
|||||
QY 481 PKAWSDLCPYDGLSEAN 498
|||||
Db 501 PKAWSDLCPYDALAEGD 518
|||||

RESULT 3
O96UT7 PRELIMINARY; PRT; 520 AA.
ID O96UT7
AC O96UT7
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Laccase B precursor (BC 1.10.3.2).
GN LAC1.
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 32745;
RA Jolivalt C., Madzak C., Caminade E., Mouglin C.;
RT "2,5-xylidine induced laccase from the basidiomycete Trametes
RL versicolor ATCC 32745.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414109; AAL07440.1; -.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
KW Oxidoreductase; Signal.
FT SIGNAL 21
SQ SEQUENCE 520 AA; 55576 MW; F3241CB929C247F9 CRC64;

Query Match 82.2%; Score 2195; DB 3; Length 520;
Best Local Similarity 79.9%; Pred. No. 1.9e-148;
Matches 398; Conservative 35; Mismatches 65; Indels 0; Gaps 0;

QY 2 IGPVASLVANAPVSPDGLRDAIVNGVVPSPPLITGKGRFQNLNVVDLTNHSMLKST 61
|||||
Db 23 IGPVADLTITNAAYSPDGSFSDRAIVVNGVVPSPPLITGKGRFQNLNVVDLTNHSMLKST 82
|||||
QY 62 SIHHGFFOAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGFWYHSHLSTQYCDGLR 121
|||||
Db 83 SIHHGFFOAGTNWADGPAFVNCQPISSGHSFLYDFQVDPDQAGFWYHSHLSTQYCDGLR 142
|||||
QY 122 GPFVYVDPKPHASRYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 181
|||||
Db 143 GPFVYVDPKPHASRYVDNVESTVITLTDWYHTAARLGRPRPLGADATVINGLGRSAST 202
|||||
QY 182 TAALAVINVQHGKRYRFLVSVISCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSIQIFA 241
|||||
Db 203 TADLSVISTVTPCKRYRFLVSVISCDPNYTFSDGHNLTAVIEVDGINSOPLLVDSIQIFA 262
|||||
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QY 242 QRYSFVLNANQTYGNTVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSTVIPLI 301
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 QRYSFVLEAQAQVNDWIRANPNFGVGTGGINSAILRYDGAANVEPTTTQTTSTAPLN 322
QY 302 ETNLHPLARMPVPGSPGVDKALNLAFNENGTNFFINNATFTPTTPVVLQILSGAQT 361
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 EVNLHPLVATAVPGSPVAGVDLAINMAFNENGTNFFINGASFTPTTPVVLQIISGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFLHGHAFVAVRSAGSTTYNDPI 421
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 AQDLLPGSVYSLPSNADIEISFPATAAAGAPHPFLHGHAFVAVRSAGSTTYNDPI 442
QY 422 FROWSTGTGAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADYKAANPVP 481
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 FROWSTGTGAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDIPDVASANPVP 502
QY 482 KAWSDLCPYDGLSEANQ 499
:||||| ||| : |||
Db 503 QAWSDLCPYDARDPSDQ 520
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RESULT 4

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Q8TG94
ID Q8TG94 PRELIMINARY; PRT; 520 AA.
AC Q8TG94;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Laccase precursor (EC 1.10.3.2).
GN CVL3.
OS Coriolus versicolor.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Coriolus.
OX NCBI_TaxID=57466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO30340;
RA Mikuni J.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO30340;
RA Iimura Y.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; D13372; BAA22153.1; -.
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase; Signal.
FT SIGNAL 1 21 POTENTIAL.
SQ SEQUENCE 520 AA; 55528 MW; F99429EEAC9D71B0 CRC64;
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Query Match 82.2%; Score 2194; DB 3; Length 520;
Best Local Similarity 79.9%; Pred. No. 2.2e-148;
Matches 398; Conservative 35; Mismatches 65; Indels 0; Gaps 0;

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QY 2 IGPVAVSLVANAPVSPDGLRDAIVNGVVPSPDLITCKGKDRFQNLNVVDLTNHSMLKST 61
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 IGPVADLTITNAAVSPDGSRAQVAVNGGTPGLITGNMGDRFQNLNVVDLTNHSMLKST 82
QY 62 SIHWGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWVHSLSTQYCDGLR 121
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 SIHWGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWVHSLSTQYCDGLR 142
QY 122 GPVWVDDPKDPHASRYDNDNESTVITLTDWYHTAARLGPREFLGADATLNGLRASSTP 181
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GPVWVDDPNDDADLDVNDNDTVITLVDWYHVAANKLGPAPFPGADATLNGLRASFTT 202
QY 182 TAALAVINVOHGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 241
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 SIHWGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWVHSLSTQYCDGLR 142
QY 122 GPVWVDDPKDPHASRYDNDNESTVITLTDWYHTAARLGPREFLGADATLNGLRASSTP 181
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GPVWVDDPNDDADLDVNDNDTVITLVDWYHVAANKLGPAPFPGADATLNGLRASFTT 202
QY 182 TAALAVINVOHGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 241
||||| ||| : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 TADLSVISVTPGKRRYRFRFLVSLSCDPNYTFSIDGHNLTVEVDGINSQPLLVDSIQIFAA 262
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RESULT 8					
Q94222 PRELIMINARY; PRT; 520 AA.					
ID	Q94222	PRELIMINARY;	PRT;	520 AA.	
AC	O94222;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DD	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DE	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)			
DI	Laccase precursor	(EC 1.10.3.2).			
DN	LCC2.				
OS	Trametes versicolor (White-rot fungus).				
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;				
QC	Aphyllophorales; Trametes.				
OX	NCBI_TaxID=5325;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=SBUG1050;				
RL	Jonsson L., Nyman P.O.;				
RA	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; Y18012; CAA77015.1; -.				
DR	InterPro: IPR001117; Cu-oxidase.				
DR	Pfam: PF00394; Cu-oxidaser.3.				
DR	PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.				
KW	Oxidoreductase; Signal.				
FT	SIGNAL 1 21	POTENTIAL.			
FT	CHAIN 22 520	LACCASE.			
SQ	SEQUENCE 520 AA; 55489 MW; 5609B4A5DF2A7D6B CRC64;				
Query Match 81.5%; Score 2176; DB 3; Length 520;					
Best Local Similarity 79.3%; Pred. No. 4.2e-147;					
Matches 395; Conservative 37; Mismatches 66; Indels 0; Gaps 0;					
QY	2	IGPVASLVVANAPVSPDGELRDATVNGVVPSPLTICKGGRFOLNVVDTLTNHSLMKST	61		
DB	23	IGPVADLTINAAVSPDGFSSQAQVVVGCTPGPLITGNMGDRFOLNVDINTDHTMLKST	82		
QY	62	SIHWGHGFQAGTWNADGPFAFVNQCPIASGHISFLYDFHFVDPQAGTFWYHSHLSTQYCDGLR	121		
DB	83	SIHWGHGFQAGTWNADGPFAFVNQCPISSGHISFLYDFHFVDPQAGTFWYHSHLSTQYCDGLR	142		
QY	122	GPFFVYDKPDPHASRYDVNDNESTVITLDWYHTAARLGPREPLGADATLINGLRGSASTP	181		
DB	143	GPFFVYDNPDAALDYDVDNDTVITLDWYHTAARLGPREPLGADATLINGLRGSASTP	202		
QY	182	TAA LAVINVQHKRYRFLYSISCDPNYTESIDGHNLTVIEVDGINSQLVDSIQIFAA	241		
DB	203	TADLTIVSVTPGKRYRFLYSISCDPNHTESIDCHNNVTIETDSINTAPLVDSIQIFAA	262		
QY	242	QRYSFVLNANOTVCNYWRANPNFGTVPFAGGINSAILRYCGAPVAPETTQTTSVIPLI	301		
DB	263	QRYSFVLEAQADVNYIRANPSFGNGFTGGINSAILRYDGAIAIEPTTTQTTSFEPLN	322		
QY	302	ETNLHLPLARMPPGSGTPPGVDKALNALAFNGFTFNINATFPPTVPVLLQLILSGAQT	361		
DB	323	EVNLHLPLAVATPCSPAAGGVDLAINNAFNENGTNFINGASTFTPVPVLLQLIIISAQN	382		
QY	362	AQDLLPAGSYVPLPAHSTIEITLPATALCAPHPFHLMGHAFVAVRSA GSTTYNNDPI	421		
DB	383	AQDLLPSSGYSLPSNADIETSFATAAAPCAPHPFHLMGHAFVAVRSA GSTTYVNDNPI	442		
QY	422	FDRVVSFTGTPAAGDNVTIRFQTDNPGPFELCHCHTDFHLDAGFAVVEADVKAANPVP	481		
DB	443	FDRVVSFTGTPAAGDNVTIRFQTDNPGPFELCHCHTDFHLDAGFAVVEADVKAANPVP	502		
QY	482	KAWSDLCPYYDGLSEANO 499			
DB	503	QAWSDLCPTYDARDPSDQ 520			
RESULT 9					
Q96TR6 PRELIMINARY; PRT; 518 AA.					
ID	Q96TR6	PRELIMINARY;	PRT;	518 AA.	
AC	Q96TR6;				

QC	Agaricales; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
QX	NCBI_TaxID=5643;
RP	SEQUENCE FROM N.A.
RR	STRAIN=PB / ATCC 200478; TISSUE=MYCELIUM;
RX	MEDLINE=98247312; PubMed=9572949;
RA	Egert C., Lafayette P.R., Temp U., Eriksson K.-E.L., Dean J.F.D.;
RT	"Molecular analysis of a laccase gene from the white rot fungus
RT	<i>Pycnoporus cinnabarinus</i> ";
RL	Appl. Environ. Microbiol. 64:1766-1772(1998).
RL	[2]
RP	SEQUENCE OF 22-42.
RC	STRAIN=PB / ATCC 200478; TISSUE=MYCELIUM;
RA	MEDLINE=97077208; PubMed=8919775;
RX	Egert C., Temp U., Eriksson K.-E.L.;
RT	"The ligninolytic system of the white rot fungus <i>Pycnoporus</i>
RT	<i>cinnabarinus</i> : purification and characterization of the laccase.";
RL	Appl. Environ. Microbiol. 62:1151-1158(1996).
CC	-1- FUNCTION: MOST PROBABLY PLAYS AN IMPORTANT ROLE IN LIGNIN
CC	DEGRADATION. CLEAVES THE C-C AND C-O BONDS OF SOME PHENOLIC LIGNIN
CC	MODEL COMPOUNDS (SUCH AS O- AND P-QUINOLS, AMINOPHENOLS AND
CC	PHENYLENEDIAMINE). MAY ALSO BE INVOLVED IN SYNTHESIS OF
CC	PHENOXAZINONE PIGMENTS.
CC	-1- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE + 2
CC	H(2)O.
CC	-1- COFACTOR: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTRES
CC	KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED
CC	BINUCLEAR (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: SECRETED.
CC	-1- INDUCTION: BY LIGNOSULFONATE, VERATRYL ALCOHOL AND 2,5-XYLIDINE.
CC	-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC	-1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
DR	EMBL: AF025481; AAC39469.1; --.
DR	InterPro: IPR001117; Cu-oxidase.
DR	Pfam: PF00394; Cu-oxidase: 3.
DR	PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
KW	Glycine reductase; Signal; Copper; Metal-binding; Lignin degradation;
KW	Oxidoprotein; Repeat; Multigene family.
FT	SIGNAL 1 21
FT	CHAIN 22 518 LACCASE.
FT	DOMAIN 23 148 PLASTOCYANIN-LIKE 1.
FT	DOMAIN 160 302 PLASTOCYANIN-LIKE 2.
FT	DOMAIN 369 489 PLASTOCYANIN-LIKE 3.
FT	METAL 85 85 COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL 87 87 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 130 130 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 132 132 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 416 416 COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL 419 419 COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL 421 421 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 471 471 COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL 472 472 COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL 473 473 COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL 477 477 COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL 482 482 COPPER (TYPE 1) (PROBABLE).
FT	CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 229 229 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 362 362 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 455 455 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE 518 AA; 55985 MW; 31B4386AFDB8DF9D CRC64;
Query Match 80.28; Score 2140; DB 3; Length 518;	
Best Local Similarity 78.38; Pred. No. 1.6e-144;	
Matches 390; Conservative 40; Mismatches 66; Indels 2; Gaps	
QY	1 AIGPVSASLVANAPSPDGFRLDAIVNGVVPSPITGKKGRFQLNVDDTLTNHSLKS 60
Dh	22 AIGPVADITLNAVSPDGFSGREAVNGVITPAPLAGQGRDFQLNVDDTLTNHPLTKT 81

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QY 61 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTQYCDGL 120
Db 82 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTQYCDGL 141
QY 121 RGFVVYDQPKDASHASRYDVNDNESTVITLTDWYHTAARLGPRLPLGADATLNGLSRSAST 180
Db 142 RGFVVYDQPKDASHASRYDVNDNESTVITLTDWYHTAARLGPRLPLGADATLNGLSRSAST 201
QY 181 PTAALAVINVQHGKRYRFRFLVSLSCDPNTFTSIDGHNLTVEIDVINSOPLLVDSIQIFA 240
Db 202 TTAADLAVIKVTOGKRYRFRFLVSLSCDPNTFTSIDGHNLTVEIDVINSOPLLVDSIQIFA 261
QY 241 AQRYSFVLNANOTVGNVYWRANPNFTGVFAGGINSAILRYOCAPVAEPTTTQTTTSVPL 300
Db 262 AQRYSFVLNANOTVGNVYWRANPNFTGVFAGGINSAILRYOCAPVAEPTTTQTTTSVPL 321
QY 301 IETNLHPLARMVPGSPTGGVDKALNLAFFNGTNGFFNNATFTPTTPVVLQILLSGAQ 360
Db 322 IETNLHPLARMVPGSPTGGVDKALNLAFFNGTNGFFNNATFTPTTPVVLQILLSGAQ 381
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLHGHAFAVVRSGASTTYNDP 420
Db 382 AAQDLVPGSVYPLPSNSSIEISFPATANAPGTPHPFHLHGHAFAVVRSGASTTYNDP 441
QY 421 IFRDVSSTGTGAAGDNVTRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 480
Db 442 IFRDVSSTGTGAAGDNVTRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 499
QY 481 PRAWSDLCPIYDGLSEAN 498
Db 500 PRAWSDLCPIYDGLSEAN 517
PRT; 518 AA.

RESULT 12
Q9UVQ2 PRELIMINARY; PRT; 518 AA.
AC Q9UVQ2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Laccase (EC 1.10.3.2).
GN LAC1.
OS Pycnopus cinnabarinus.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllum; Pycnopus.
OX NCBI_TaxID=5643;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I-937;
RA Moukha S., Otterbein L., Record E.;
RT "Cloning, characterization and expression of the gene encoding an
RT extracellular laccase from Pycnopus cinnabarinus I-937 strain; an
RT allele showing a great divergence at the nucleic acid level with the
RT Lcc 3-1 gene of Strain ATCC 200478."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=I-937;
RA Otterbein L., Record E., Moukha S.;
RT "Cloning of a cDNA encoding laccase protein from Pycnopus
RT cinnabarinus I-937."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF170093; AAF13052.1;
DR EMBL: AF152170; AAG13724.1;
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase.
SQ SEQUENCE 518 AA; 56292 MW; 329714CF463ED081 CRC64;
```

Query Match 80.1%; Score 2138; DB 3; Length 518;
Best Local Similarity 77.7%; Pred. NO. 2.2e-144;
Matches 387; Conservative 44; Mismatches 65; Indels 2; Gaps 1;

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QY 1 AIGPVAASLVVANAPSPDGLRDAIVVNGVPSPLITGKGRFQNLNVVDLTNHSMLKS 60
Db 22 AIGPVAASLVVANAPSPDGLRDAIVVNGVPSPLITGKGRFQNLNVVDLTNHSMLKS 81
QY 61 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTQYCDGL 120
Db 82 TSIHWHGFFQAGTNWADGPAFVNCQPIASGHSFLYDFHVPDQAGTWFYHSHLSLSTQYCDGL 141
QY 121 RGFVVYDQPKDASHASRYDVNDNESTVITLTDWYHTAARLGPRLPLGADATLNGLSRSAST 180
Db 142 RGFVVYDQPKDASHASRYDVNDNESTVITLTDWYHTAARLGPRLPLGADATLNGLSRSAST 201
QY 181 PTAALAVINVQHGKRYRFRFLVSLSCDPNTFTSIDGHNLTVEIDVINSOPLLVDSIQIFA 240
Db 202 TTAADLAVIKVTOGKRYRFRFLVSLSCDPNTFTSIDGHNLTVEIDVINSOPLLVDSIQIFA 261
QY 241 AQRYSFVLNANOTVGNVYWRANPNFTGVFAGGINSAILRYOCAPVAEPTTTQTTTSVPL 300
Db 262 AQRYSFVLNANOTVGNVYWRANPNFTGVFAGGINSAILRYOCAPVAEPTTTQTTTSVPL 321
QY 301 IETNLHPLARMVPGSPTGGVDKALNLAFFNGTNGFFNNATFTPTTPVVLQILLSGAQ 360
Db 322 IETNLHPLARMVPGSPTGGVDKALNLAFFNGTNGFFNNATFTPTTPVVLQILLSGAQ 381
QY 361 TAQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLHGHAFAVVRSGASTTYNDP 420
Db 382 AAQDLVPGSVYPLPSNSSIEISFPATANAPGTPHPFHLHGHAFAVVRSGASTTYNDP 441
QY 421 IFRDVSSTGTGAAGDNVTRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 480
Db 442 IFRDVSSTGTGAAGDNVTRFOTDNPFPWFLHCHIDFHLDAFAIVFAEDVADVKAANPV 499
QY 481 PRAWSDLCPIYDGLSEAN 498
Db 500 PRAWSDLCPIYDGLSEAN 517
PRT; 524 AA.

RESULT 13
Q13422 PRELIMINARY; PRT; 524 AA.
AC Q13422:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Phenoloxidase (EC 1.10.3.2).
GN POX3.
OS basidiomycete CECT 20197.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Polyporaceae.
OX NCBI_TaxID=51095;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 20197;
RX MEDLINE=97355933; PubMed=9212414;
RA Mansur M., Suarez T., Fernandez-Larrea J.B., Brizuela M.A.,
RT "Identification of a laccase gene family in the new lignin-degrading
RT basidiomycete CECT 20197."
RL Appl. Environ. Microbiol. 63:2637-2646(1997).
DR EMBL: U55401; AAB63445.1;
DR HSSP: P37064; IAOZ.
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
KW Oxidoreductase.
SQ SEQUENCE 524 AA; 56240 MW; 490BFA4AB1168608 CRC64;
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Best Local Similarity 77.8%; Pred. NO. 2.6e-144;
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Qy 121 RGPVVYDQKDPHASRYDVNDNESTVITLTDWYHTAARLGRPRPLGADATLINGLGRSAST 180
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DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
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GN LCC3-1.
OS Polyporus ciliatus.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Polyporaceae; Polyporus.
OX NCBI_TaxID=134555;
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RP SEQUENCE FROM N.A.
RC STRAIN=TH1; TISSUE=VEGETATIVE MYCELIA;
RA Schnee C., Eggert C.;
RT "Isolation and characterization of three laccase genes from the white-
rot fungus Polyporus ciliatus and their expression during fruiting.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF176230; AAG09229.1; .
DR HSP; P37064; IAOZ.
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DR Pfam; PF00394; Cu-oxidase; 3.
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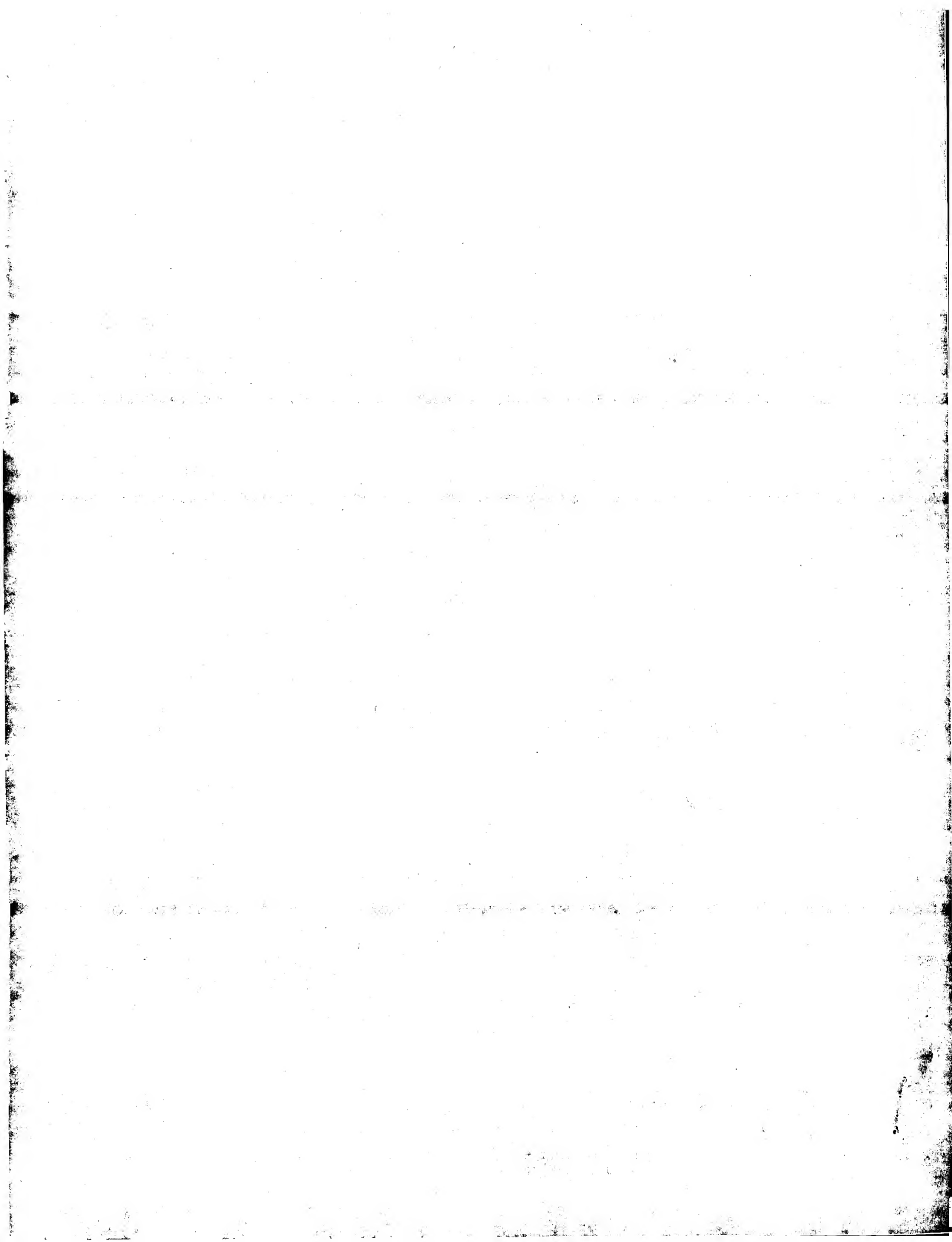
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DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Billirubin oxidase precursor.
OS Trachyderma tsunodae.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cuculiformia; Tenebrionidae; Trachyderma.
OX NCBI_TaxID=65050;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-2593;
RA Iwamoto H., Watanabe H., Minakami M., Hirose J., Hiroki K., Mukai H.,
RA Yoshioka H., Kato I.;
RT "Purification, Characterization, and Molecular Cloning of Billirubin
Oxidase from Trachyderma tsunodae K-2593.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB006824; BAA28668.1; .
DR InterPro; IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 521 AA; 56456 MW; ED078214DD2986D4 CRC64;

Query Match 79.0%; Score 2107.5; DB 5; Length 521;
Best Local Similarity 77.0%; Pred. No. 3.3e-142;
Matches 384; Conservative 44; Mismatches 70; Indels 1; Gaps 1;

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Qy 62 TSIHWHGFFQAGTNWADGPAFVNCPIASGHSFLYDFHPDQAGTFWYHSHLSQYCDGL 121
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QY 122 GPFWVYDKPHASRYDVNDNESTVITLTDWYHTAARLGPFPPLGADATLINGLGRSASTP 181
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Search completed: December 14, 2002, 08:27:58
Job time : 89 secs



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OM protein - protein search, using sw model

Run on: December 14, 2002, 08:25:32 ; Search time 27 seconds
(without alignments)
543.779 Million cell updates/sec

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Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2656	99.5	499	4	US-09-399-886-3
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5	2656	99.5	499	4	US-09-576-281-3
6	2656	99.5	519	1	US-08-462-484-4
7	2656	99.5	519	1	US-08-441-147-4
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ALIGNMENTS

RESULT 1
US-09-032-315-3
; Sequence 3, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59858180 No. 5985818disk of No. 5985818th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,315
; FILING DATE: 27-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-032-315-3

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Best Local Similarity 99.4%; Pred. No. 7.7e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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RESULT 2

US-08-993-318A-3
; Sequence 3, Application US/08993318A
; Patent No. 5998353
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59983530 No. 5998353disk of No. 5998353th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,318A
; FILING DATE: December 18, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 5032.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-993-318A-3
Query Match 99.5%; Score 2656; DB 2; Length 499;
Best Local Similarity 99.4%; Pred. No. 7-7e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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RESULT 3

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; Sequence 3, Application US/09399886
; Patent No. 6140092
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6140092o No. 6140092disk of No. 6140092th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/399,886
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,318

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: FILING DATE: December 18, 1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Gregg, Valeta A.
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 5032.200-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 499 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-399-886-3

Query Match          99.5%; Score 2656; DB 4; Length 499;
Best Local Similarity 99.4%; Pred. No. 7.7e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db   1 AIGPVASLVVANAPVSPDGFURDAIVVGVVPSPLITGKKGDRFQLNVVDTLTNHSM LKS 60
    |||||
QY  61 TSIHHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
    |||||
Db   61 TSIHHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
    |||||
QY  121 RGPVYVYDPKDPHASRYDVDNESVITLTDWYHTAARLGPFPGLCADATLINGLGRSAST 180
    |||||
Db   121 RGPVYVYDPKDPHASRYDVDNESVITLTDWYHTAARLGPFPGLCADATLINGLGRSAST 180
    |||||
QY  181 PTAALAVINVOHGKRYRFLVSIISCDPNYTFSDIGHNLTVTIEVDGINSQPLLVSQIIFA 240
    |||||
Db   181 PTAALAVINVOHGKRYRFLVSIISCDPNYTFSDIGHNLTVTIEVDGINSQPLLVSQIIFA 240
    |||||
QY  241 AQRYSFVLNANQTVGNVYWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSVIPL 300
    |||||
Db   241 AQRYSFVLNANQTVGNVYWRANPNFGTVGFAGGINSAILRYOGAPVAEPTTTQTTSVIPL 300
    |||||
QY  301 IETNLHPLARMPVPGSPTPGGVDKALNAFNFGTNEFINNATPTPPVPVLLQLLSGAQ 360
    |||||
Db   301 IETNLHPLARMPVPGSPTPGGVDKALNAFNFGTNEFINNATPTPPVPVLLQLLSGAQ 360
    |||||
QY  361 TAQDLLPAGSYVPLPAHSTTIEITLPATALAPGAPHPHLHGFAFVRSAGSTTYNYNDP 420
    |||||
Db   361 TAQDLLPAGSYVPLPAHSTTIEITLPATALAPGAPHPHLHGFAFVRSAGSTTYNYNDP 420
    |||||
QY  421 IFRVYVSTGTPAAGDNVTYIRQTDPNGPFWLCHHIDFHLDAAGFAIVFAEDVADYKAANPV 480
    |||||
Db   421 IFRVYVSTGTPAAGDNVTYIRQTDPNGPFWLCHHIDFHLDAAGFAIVFAEDVADYKAANPV 480
    |||||
QY  481 PKAWSDLCPYDGLSEANQ 499
    |||||
Db   481 PKAWSDLCPYDGLSEANQ 499
    |||||

RESULT 4
US-09-396-260-3
: Sequence 3, Application US/09396260
: Patent No. 6184015
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: APPLICANT: Xu, Feng
: TITLE OF INVENTION: LACCASE MUTANTS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 61840150 No. 61840150disk of No. 6184015th America, Inc.
: STREET: 405 Lexington Avenue
: CITY: New York
: STATE: NY

```

; Sequence 3, Application US/09576281
; Patent No. 6277611
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: No. 6277611o No. 6277611disk of No. 6277611th America
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/576,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,318
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 5032.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-576-281-3

Query Match 99.5%; Score 2656; DB 4; Length 499;
Best Local Similarity 99.4%; Pred. No. 7.7e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPVSPDGFRLDAIVVNGVYVPSPLITGKGRFQLNVVDLTNHSMLKS 60
Db 1 AIGPVASLVVANAPVSPDGFRLDAIVVNGVYVPSPLITGKGRFQLNVVDLTNHSMLKS 60

QY 61 TSIHWGFFOAGTNWADGPAFVNCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 61 TSIHWGFFOAGTNWADGPAFVNCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120

QY 121 RGFVVYDVKDPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSAST 180
Db 121 RGFVVYDVKDPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSAST 180

QY 181 PTAALAVINVQHGRYRFRVLVSICDPNTFTSIDGHNLTAVIEVDGINSQPLLVDSIQIFA 240
Db 181 PTAALAVINVQHGRYRFRVLVSICDPNTFTSIDGHNLTAVIEVDGINSQPLLVDSIQIFA 240

QY 241 AQRYSFVLNANQTVGNVWRANFNFTGVPAGGINSAILRYQCAPVAEPTTTQTTSVIPL 300
Db 241 AQRYSFVLNANQTVGNVWRANFNFTGVPAGGINSAILRYQCAPVAEPTTTQTTSVIPL 300

QY 301 IETNLHPLARMPVPGSPGCGVDKALNLAFTNFTNFINNAFTPTPTVPLVLIQILSGAQ 360
Db 301 IETNLHPLARMPVPGSPGCGVDKALNLAFTNFTNFINNAFTPTPTVPLVLIQILSGAQ 360

QY 361 TAODLLPAGSVYPLPAHSTIEITLPATAPAGAPHPFHLHGHAFAVVRSGSTTYNNDP 420
Db 361 TAODLLPAGSVYPLPAHSTIEITLPATAPAGAPHPFHLHGHAFAVVRSGSTTYNNDP 420

QY 421 IFRDVVSTGTTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDDAGFAIVFAEDVADVKAANPV 480
Db 421 IFRDVVSTGTTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDDAGFAIVFAEDVADVKAANPV 480

QY 481 PKAWSDLCPYDGLSEANQ 499
Db 481 PKAWSDLCPYDGLSEANQ 499

RESULT 6
US-08-462-484-4
; Sequence 4, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboe, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-484-4

Query Match 99.5%; Score 2656; DB 1; Length 519;
Best Local Similarity 99.4%; Pred. No. 8.1e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AIGPVASLVVANAPVSPDGFRLDAIVVNGVYVPSPLITGKGRFQLNVVDLTNHSMLKS 60
Db 21 AIGPVASLVVANAPVSPDGFRLDAIVVNGVYVPSPLITGKGRFQLNVVDLTNHSMLKS 80

QY 61 TSIHWGFFOAGTNWADGPAFVNCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 81 TSIHWGFFOAGTNWADGPAFVNCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 140

QY 121 RGFVVYDVKDPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSAST 180

|||||
Db 141 RGFVVYDPKDPHASKRYDVNDNESTVITLTDWYHTAARLGPKEPLGADATLINGLRSAST 200
QY 181 PTAALAVINVQHGKRYRRLVSIISCDPNYTFISIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Db 201 PTAALAVINVQHGKRYRRLVSIISCDPNYTFISIDGHNLTVEVDGINSQPLLVDSIQIFA 260
QY 241 AQRYSEVLNANQTVGNVWRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
Db 261 AQRYSEVLNANQTVGNVWRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 320
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 360
Db 321 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 380
QY 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 420
Db 381 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 440
QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 500
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 501 PKAWSDLCPYDGLSEANQ 519

RESULT 7

US-08-441-147-4
; Sequence 4, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441.147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-147-4

Query Match 99.5%; Score 2656; DB 1; Length 519;

Best Local Similarity 99.4%; Pred. No. 8.1e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 AIGPVASIVVANAPVSPDGFRLDAIVAGVVPSPITLTKGKDRFQLNVVYDTLTNHSMLKS 60
Db 21 AIGPVASIVVANAPVSPDGFRLDAIVAGVVPSPITLTKGKDRFQLNVVYDTLTNHSMLKS 80
QY 61 TSIHHGTFQAGTNWADGPAFVNCQPIASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
Db 81 TSIHHGTFQAGTNWADGPAFVNCQPIASGHSLYDFHVPDQAGTFWYHSHLSTQYCDGL 140
QY 121 RGFVVYDPKDPHASKRYDVNDNESTVITLTDWYHTAARLGPKEPLGADATLINGLRSAST 180
Db 141 RGFVVYDPKDPHASKRYDVNDNESTVITLTDWYHTAARLGPKEPLGADATLINGLRSAST 200
QY 181 PTAALAVINVQHGKRYRRLVSIISCDPNYTFISIDGHNLTVEVDGINSQPLLVDSIQIFA 240
Db 201 PTAALAVINVQHGKRYRRLVSIISCDPNYTFISIDGHNLTVEVDGINSQPLLVDSIQIFA 260
QY 241 AQRYSEVLNANQTVGNVWRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 300
Db 261 AQRYSEVLNANQTVGNVWRANPNFCTVGFAGGINSAILRYOGAPVAEPTTTQTSVIPL 320
QY 301 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 360
Db 321 IETNLHPLARMPVPGSPPTGGVDKALNLAFAFNENFTINNATFTPTVPVLLQLLSGAQ 380
QY 361 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 420
Db 381 TAQDLLPAGSVYPLPAHSTIETLPTALAPGAPHPFHLHGHAFAVRSAGSTTNYNDP 440
QY 421 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVVSTGTPAAGDNVTIRFQTDNPGPWFHLCHIDFHLDAAGFAIVFAEDVADVKAANPV 500
QY 481 PKAWSDLCPYDGLSEANQ 499
Db 501 PKAWSDLCPYDGLSEANQ 519

RESULT 8
PCT-US95-07536-4
; Sequence 4, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07536
; FILING DATE: 15-June-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/265,534
; FILING DATE: 24-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07536-4

Query Match      99.5%; Score 2656; DB 5; Length 519;
Best Local Similarity 99.4%; Pred. No. 8.1e-231;
Matches 496; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AIGVASLVVANAPVSPDGLRDAIVVGVVPSPLITGKKGDRFQLNVVDLTNHSMLKS 60
Db 21 AIGVASLVVANAPVSPDGLRDAIVVGVVPSPLITGKKGDRFQLNVVDLTNHSMLKS 80

Qy 61 TSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 120
Db 81 TSIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL 140

Qy 121 RGPVVYDPRKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSAST 180
Db 141 RGPVVYDPRKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSAST 200

Qy 181 PTAALAVINVQHGKRYRFLRVSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSTQIFA 240
Db 201 PTAALAVINVQHGKRYRFLRVSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSTQIFA 260

Qy 241 AQRYSFVLNANOTVGNVWVRANPNFGTVGFAGGINSAILRYQGAPVAEPTTQTTTSVIPL 300
Db 261 AQRYSFVLNANOTVGNVWVRANPNFGTVGFAGGINSAILRYQGAPVAEPTTQTTTSVIPL 320

Qy 301 IETNLHPLARMPVPGSPTPGGVKALNLAFFNNGTFFINNATFTPTPVLLQILSGAQ 360
Db 321 IETNLHPLARMPVPGSPTPGGVKALNLAFFNNGTFFINNATFTPTPVLLQILSGAQ 380

Qy 361 TAQDLLPAGSVYPLPAHSTIETLTPATALAPGAPPHLGHAFVAVRSAGSTTYNDP 420
Db 381 TAQDLLPAGSVYPLPAHSTIETLTPATALAPGAPPHLGHAFVAVRSAGSTTYNDP 440

Qy 421 IFRDVSTGTGAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 480
Db 441 IFRDVSTGTGAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 500

Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 501 PKAWSDLCPYDGLSEANQ 519

RESULT 9
US-09-032-315-2
; Sequence 2, Application US/09032315
; Patent No. 5985818
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 5985818 of No. 5985818disk of No. 5985818th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,315
; FILING DATE: 27-FEB-1998
; CLASSIFICATION:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-032-315-2

Query Match      82.5%; Score 2201; DB 2; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;

Qy 2 IGPVASLVVANAPVSPDGLRDAIVVGVVPSPLITGKKGDRFQLNVVDLTNHSMLKST 61
Db 2 IGPVADLTITNAAVSPDGSFQAVVNGVTPGLITGNGMDRQLNVLDNLNHTMLKST 61

Qy 62 SIHHGFFQAGTNWADGPAFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Db 62 SIHHGFFQAGTNWADGPAFVNOCPITSSGHSFLYDFQVDPQAGTFWYHSHLSTQYCDGLR 121

Qy 122 GPFVYDPRKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSASTP 181
Db 122 GPFVYDPRKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLINGLRSASTP 181

Qy 182 TAALAVINVQHGKRYRFLRVSISCDPNYTFSDGHNLTVIEVDGINSQPLLVDSTQIFA 241
Db 182 TADLSVISTPGRKRYRFLRVSLSCDPNYTFSDGHNNTIETDSINTAPLVDSTQIFA 241

Qy 242 QRYSEVLNANOTVGNVWVRANPNFGTVGFAGGINSAILRYQGAPVAEPTTQTTTSVIPLI 301
Db 242 QRYSEVLNANOTVGNVWVRANPNFGTVGFAGGINSAILRYDGAANAEPVTTQTTSTAPLN 301

Qy 302 ETNLHPLARMPVPGSPTPGGVKALNLAFFNNGTFFINNATFTPTPVLLQILSGAQ 361
Db 302 EVNLHPLVTTAVPGSPVAGGVDLAINMAFNNGTFFINGASFTPTPTPVLLQILSGAQ 361

Qy 362 AQDLLPAGSVYPLPAHSTIETLTPATALAPGAPPHLGHAFVAVRSAGSTTYNDPI 421
Db 362 AQDLLPAGSVYPLPSNADIEISFATAAPGAPPHLGHAFVAVRSAGSTTYNDPI 421

Qy 422 FRDVSTGTGAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 481
Db 422 FRDVSTGTGAAGDNVTIRFQTDNPGFWFLHCHIDFHLDAAGFAIVFAEDVADVKAANPV 481

Qy 482 KAWSDLCPYDGLSEANQ 499
Db 482 QAWSDLCPYDGLDPSDQ 499

RESULT 10
US-08-993-318A-2
; Sequence 2, Application US/08993318A
; Patent No. 5998353
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Palle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Chery, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 5998353 of No. 5998353disk of No. 5998353th America
; STREET: 405 Lexington Avenue
; CITY: New York
```

COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,318A
FILING DATE: December 18, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-318A-2

Query Match 82.5%; Score 2201; DB 2; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
Qy 2 IGPVSLVAVNAPSPDGLRDAIVVNGVWSPDLITGKKGDRFQNLVNDLTNNHMLKST 61
Db 2 IGPVADLTITNAVSPDGSFQAVVNGGTGPLITGNMGDRFQNLVNDLTNNHMLKST 61
Qy 62 SIHWHGFFQAGTNWADGPAFVNOCPVSIAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Db 62 SIHWHGFFQKGTNADGPAFVNOCPVSIAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Qy 122 GFVVYDPKPHASRYDVNDNESTVITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Db 122 GFVVYDPNDPAADLYDVNDNDVTITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Qy 182 TAALAVINVOHGKRYRFRFLVSLSCDPNVTFSIDGHNLFVIEVDGINSOPLVDSIQIFAA 241
Db 182 TAALAVINVOHGKRYRFRFLVSLSCDPNVTFSIDGHNLFVIEVDGINSOPLVDSIQIFAA 241
Qy 302 ETNLHPLARMVPVGSPTPGGVKALNLAFFNFTNNATFTPTVPVLLQILSGAQT 361
Db 302 EVNLHPLVTTAVPGSPVAGGVLDLAINMAFNFTNGFTNGASFTPTVPVLLQILSGAQT 361
Qy 362 AQDILLPGSVYSLPSNADIEISFPATAAAGPAPHFHLRHGAFVAVRSAGSTVYNDNPI 421
Db 362 AQDILLPGSVYSLPSNADIEISFPATAAAGPAPHFHLRHGAFVAVRSAGSTVYNDNPI 421
Qy 422 FRDVTSTCTPAAGNVITRFOTDNGPWFHLCHIDFHLDAFAIVAEADVAAANVPV 481
Db 422 FRDVTSTCTPAAGNVITRFOTDNGPWFHLCHIDFHLDAFAIVAEADVAAANVPV 481
Qy 482 KAWSDLCPYDGLSEANQ 499
Db 482 KAWSDLCPYDGLSEANQ 499

RESULT 11
us-09-399-886-2
; Sequence 2, Application US/09399886
; Patent No. 6140092

GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
APPLICANT: Svendsen, Allan
APPLICANT: Schneider, Palle
APPLICANT: Rasmussen, Grethe
APPLICANT: Cherry, Joel
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400920 No. 6140092disk of No. 6140092th America
STREET: 405 Lexington Avenue
CITY: New York
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/399,886
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,318
FILING DATE: December 18, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-399-886-2

Query Match 82.5%; Score 2201; DB 4; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
Qy 2 IGPVSLVAVNAPSPDGLRDAIVVNGVWSPDLITGKKGDRFQNLVNDLTNNHMLKST 61
Db 2 IGPVADLTITNAVSPDGSFQAVVNGGTGPLITGNMGDRFQNLVNDLTNNHMLKST 61
Qy 62 SIHWHGFFQAGTNWADGPAFVNOCPVSIAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Db 62 SIHWHGFFQKGTNADGPAFVNOCPVSIAGSHSFLYDFHVPDQAGTFWYHSHLSTQYCDGLR 121
Qy 122 GFVVYDPKPHASRYDVNDNESTVITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Db 122 GFVVYDPNDPAADLYDVNDNDVTITLDWYHTAARLGPREFPLGADATLNLGKRSASTP 181
Qy 182 TAALAVINVOHGKRYRFRFLVSLSCDPNVTFSIDGHNLFVIEVDGINSOPLVDSIQIFAA 241
Db 182 TAALAVINVOHGKRYRFRFLVSLSCDPNVTFSIDGHNLFVIEVDGINSOPLVDSIQIFAA 241
Qy 242 QRYSFVLNANQVGNVWRANPNFCTGVFAGGINSAILRYOGAPVAEPTTTQTTSTAPLN 301
Db 242 QRYSFVLEANOAVDNYWRANPNFCTGVFAGGINSAILRYOGAPVAEPTTTQTTSTAPLN 301
Qy 302 ETNLHPLARMVPVGSPTPGGVKALNLAFFNFTNNATFTPTVPVLLQILSGAQT 361
Db 302 EVNLHPLVTTAVPGSPVAGGVLDLAINMAFNFTNGFTNGASFTPTVPVLLQILSGAQT 361
Qy 362 AQDILLPGSVYSLPSNADIEISFPATAAAGPAPHFHLRHGAFVAVRSAGSTVYNDNPI 421
Db 362 AQDILLPGSVYSLPSNADIEISFPATAAAGPAPHFHLRHGAFVAVRSAGSTVYNDNPI 421

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Db 362 AODLLPGSVYSLPSNADIEISPPATAAAPGAPHPHLLHGHAFVAVVRSAGSVYNDNPI 421
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QY 482 KAWSDLCPYDGLSEANQ 499
Db 482 QAWSDLCPYDALDPSDQ 499

RESULT 12
US-09-396-260-2
; Sequence 2, Application US/09396260
; Patent No. 6184015
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Xu, Feng
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6184015th No. 6184015disk of No. 6184015th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/396,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,315
; FILING DATE: 27-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 5200.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-396-260-2
Query Match 82.5%; Score 2201; DB 4; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;

QY 2 IGPVAVSLVAVAPSPDGLRDAIVVNGVVPSPILITKGGDRFQINLVVDLTINHSMLKST 61
Db 2 IGPVADLTITAAVSPDGSFQAVVNGVGTGPGLTGNGMGRFQINLVVDLTINHSMLKST 61
QY 62 SIHWGFFQAGTNWADGPAFVNOCPVAGSHSFLYDFHVPDQAGTFWYHSHLSSTQVCDGLR 121
Db 62 SIHWGFFQAGTNWADGPAFVNOCPVAGSHSFLYDFHVPDQAGTFWYHSHLSSTQVCDGLR 121
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Db 122 GPFVYVDPKPHASRYVDNVESTVITLTDWYHTAARLGRPFLGADATFLINGLRSASTP 181
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Db 162 TRAAVAVNQHKRYRFRFLVSLSCDPNTTFSIDGNMTIETDINTAPLVVDSIQIFAA 241
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Db 242 QRYSFVLNANQTVGNWVRANENFNTVGFAGINSAILRYQGAPVAEPTTTTSTVIPLI 301
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Db 302 EYNLHPLVTTAVPGSPVAGGVDLAINMAFNFGTFFINATFTPTTVPVLQILSGAQT 361
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Db 362 AODLLPAGSVYSLPSNADIEISPPATAAAPGAPHPHLLHGHAFVAVVRSAGSVYNDNPI 421
QY 422 FRDVSSTGTPAAGDNTVIRFQDNPFGWFLHCHIDHLDAGFAIVFAEDVADVKAANPVP 481
Db 422 FRDVSSTGTPAAGDNTVIRFQDNPFGWFLHCHIDHLDAGFAIVFAEDVADVKAANPVP 481
QY 482 KAWSDLCPYDGLSEANQ 499
Db 482 QAWSDLCPYDALDPSDQ 499

RESULT 13
US-09-576-281-2
; Sequence 2, Application US/09576281
; Patent No. 6277611
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Svendsen, Allan
; APPLICANT: Schneider, Falle
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: LACCASE MUTANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6277611th No. 6277611disk of No. 6277611th America
; STREET: 405 Lexington Avenue
; CITY: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/576,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,318
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 5032.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-576-281-2
Query Match 82.5%; Score 2201; DB 4; Length 499;
Best Local Similarity 80.1%; Pred. No. 7.1e-190;
Matches 399; Conservative 35; Mismatches 64; Indels 0; Gaps 0;
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QY 2 IGPVSLVAVANAPVSPDGLRDAIVVNGVVPSPPLITGKKGDRFQNLNVDTLTHSHMLKST 61
Db 2 IGPVADLITNAVSPDGFSGRAVAVVNGTGPPLITGNMGDRFQNLNVDTLTHSHMLKST 61
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Db 62 SIHWGFFQAGTNWADGPAFVNOCPISGHSFLYDFHPVDAQAGTFWYHSHLSQYCDGLR 121
QY 122 GFVVYDPKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLNLGGRSASTP 181
Db 122 GFVVYDNDPAADLYDVNDNDVTITLVDWYHVAALGPAFPLGADATLNLGGRSPST 181
QY 182 TAALAVINQHGKRYRFLVSLSCDPNTFSIDGHNLTVEIDGINSQPLLVDSIQIFAA 241
Db 182 TADLSVISVTPCKRYRFLVSLSCDPNTFSIDGHNWLTIEDSINTAPLVVDSIQIFAA 241
QY 242 QRYSVLNAVOTVGNVWRANPFGTVGAGGINSAILRYQGAPVAEPTTTQTSVPLI 301
Db 242 QRYSEVLEAQAVDNYWIRANPNFNGVGTGGINSAILRYDCAAAVEPTTTQTSAPLN 301
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Db 302 EYNLHPLVTTAVPGSPVAGGVDLAINMAFNFGTFFINGASFTPTVPVLLQIISGAQN 361
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLGHAFVAVRSAGSTTYNDPI 421
Db 362 AQDLLPSGVYSLPSNADIEISFPATAAAGAPHPFHLGHAFVAVRSAGSTVYNDNPI 421
QY 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDHLDAGFAIVFAEDVADVKAANVP 481
Db 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDHLDHLEAGFAIVFAEDIPDVASANVP 481
QY 482 KAWSDLCPYDGLSEANQ 499
Db 482 QAWSDLCPYDALDPSDQ 499

RESULT 14
US-08-462-484-2
; Sequence 2, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Iaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56675310 No. 5667531th disk of No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
```

```
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus
;
US-08-462-484-2

Query Match 82.2%; Score 2194; DB 1; Length 520;
Best Local Similarity 79.7%; Pred. No. 3.2e-189;
Matches 397; Conservative 36; Mismatches 65; Indels 0; Gaps 0;

QY 2 IGPVSLVAVANAPVSPDGLRDAIVVNGVVPSPPLITGKKGDRFQNLNVDTLTHSHMLKST 61
Db 23 IGPVADLITNAVSPDGFSGRAVAVVNGTGPPLITGNMGDRFQNLNVDTLTHSHMLKST 82
QY 62 SIHWGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHPVDAQAGTFWYHSHLSQYCDGLR 121
Db 83 SIHWGFFQAGTNWADGPAFVNOCPISGHSFLYDFHPVDAQAGTFWYHSHLSQYCDGLR 142
QY 122 GFVVYDPKPHASRYDVNDNESTVITLTDWYHTAARLGRPFPLGADATLNLGGRSASTP 181
Db 143 GFVVYDNDPAADLYDVNDNDVTITLVDWYHVAALGPAFPLGADATLNLGGRSPST 202
QY 182 TAALAVINQHGKRYRFLVSLSCDPNTFSIDGHNLTVEIDGINSQPLLVDSIQIFAA 241
Db 203 TADLSVISVTPCKRYRFLVSLSCDPNTFSIDGHNWLTIEDSINTAPLVVDSIQIFAA 262
QY 242 QRYSVLNAVOTVGNVWRANPFGTVGAGGINSAILRYQGAPVAEPTTTQTSVPLI 301
Db 263 QRYSEVLEAQAVDNYWIRANPNFNGVGTGGINSAILRYDCAAAVEPTTTQTSAPLN 322
QY 302 ETNLHPLARMPVPGSPTPGVDKALNLAENFNGTFFINNTFTPTVPVLLQILSGAQT 361
Db 323 EYNLHPLVTTAVPGSPVAGGVDLAINMAFNFGTFFINGASFTPTVPVLLQIISGAQN 382
QY 362 AQDLLPAGSVYPLPAHSTIEITLPATALAPGAPHPFHLGHAFVAVRSAGSTTYNDPI 421
Db 383 AQDLLPSGVYSLPSNADIEISFPATAAAGAPHPFHLGHAFVAVRSAGSTVYNDNPI 442
QY 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDHLDAGFAIVFAEDVADVKAANVP 481
Db 443 FRDVTSTGTPAAGDNVTIRFQTDNPGPWLHCHIDHLDHLEAGFAIVFAEDIPDVASANVP 502
QY 482 KAWSDLCPYDGLSEANQ 499
Db 503 QAWSDLCPYDALDPSDQ 520

RESULT 15
US-08-441-147-2
; Sequence 2, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Iaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57704180 No. 5770418th disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
```

STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,147
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Polyporus pinsitus
PS-08-441-147-2

Query Match	82.2%	Score	2194;	DB 1;	Length	520;			
Best Local Similarity	79.7%;	Pred. No.	3.2e-189;						
Matches	397;	Conservative	36;	Mismatches	65;	Indels	0;	Gaps	0;

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Qy	23	IGPVADITITNAAV	SPDGF	SQAVV	VNGP	PGPLIT	GNMGDRFOLNID	LTNHTMVKST	82				
Db			:	:	:								
Qy	62	SIHHGFFQAGTN	WADGPAF	VNOC	PIASGHS	FLYDF	HWPDQAGFWY	SHSLSTQYCDGLR	121				
Db			:	:	:								
Qy	83	SIHHGFFQKGT	NWADGPAF	INOC	PISSGHS	FLYDF	QVDPQAGFWY	SHSLSTQYCDGLR	142				
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Qy	122	GPVVYDPKDP	HASRYDV	DN	ESTVIT	ITDMVHT	TAARLGRPR	PLGADATLINGLGRSASTP	181				
Db			:	:	:								
Qy	143	GPVVYDNP	DEPAADLY	DV	DNDDT	ITVLVDW	THVAAKLG	PAPPLGADATLINGKGRSPST	202				
Db			:	:	:								
Qy	182	TAALAVINVO	HGKRYR	FLR	LYSIS	CDPN	YTSIDGHN	LTVEOGINSOP	LLVDSIQIFAA	241			
Db			:	:	:								
Qy	203	TADLSVLSV	TPGKRYR	FLR	LYS	LSCD	PNYTSIDGHN	MTIETDSINTAP	LVVDSIQIFAA	262			
Db			:	:	:								
Qy	242	QRYSFVLN	ANO	TGVNY	WVRAN	PNFTG	YFAGGINS	ALLRYOGA	SVAEPTTTQTTSV	301			
Db			:	:	:								
Qy	263	QRYSFVLE	ANQAV	DYNI	WRAN	PNFGN	VGFTGG	INSA	ILRYDGA	AVEPTTTQTTSAPLN	322		
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Qy	302	ETNHLPL	ARM	PV	PGSP	TPGGV	DKALN	IAFN	ENGTFN	FINNATFTPPV	VLQILSGAQT	361	
Db			:	:	:								
Qy	323	EVNHLPL	VTAV	PGSP	VAGGY	VDLAIN	MAFN	ENGTFN	FTSTPT	TPVVLQIISGAQN	382		
Db			:	:	:								
Qy	362	AQDLLPAG	SVYPL	PAHST	ETITL	PAT	ALAP	GAHP	PHLGH	HAFVAVRSAG	STTYNNDPI	421	
Db			:	:	:								
Qy	383	AQDLLP	SGSV	YLS	PSNAD	IELSF	PATA	APGAP	PHFHL	HGHAFVAVRSAG	STTYNNDPI	442	
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Qy	422	FRDYYSTGT	PAAGDN	VTIR	FQ	TDPN	PGPW	FLCH	IDF	HL	DAGFAIV	FADVADVKAANPVP	481
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Qy	443	FRDYYSTGT	PAAGDN	VTIR	FQ	TDPN	PGPW	FLCH	IDF	HL	EAGFAIV	FADVADVKAANPVP	502
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Qy	482	KAWSDL	CPYD	GL	SEANQ	499							
Db			:	:	:								
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Db			:	:	:								

Search completed: December 14, 2002, 08:29:50
Job time : 29 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:07:51 ; Search time 60 Seconds
(without alignments)
7666.919 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gcatcgccgctggcgcag.....tgagcaggactaacagtgta 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	771.8	51.5	2880	1	US-08-441-147-3
3	771.8	51.5	2880	5	PCT-US95-07536-3
4	519	34.6	1722	4	US-09-221-275-3
5	472.6	31.5	1170	3	US-08-689-421-20
6	472.6	31.5	1170	4	US-09-389-528-20
7	472.6	31.5	1170	4	US-09-181-827A-20
8	452.8	30.2	2418	1	US-08-462-484-1
9	452.8	30.2	2418	1	US-08-441-147-1
10	452.8	30.2	2418	5	PCT-US95-07536-1
11	439.6	29.3	1161	3	US-08-689-421-22
12	439.6	29.3	1161	4	US-09-389-528-22
13	439.6	29.3	1161	4	US-09-181-827A-22
14	377.6	25.2	1176	3	US-08-689-421-18
15	377.6	25.2	1176	4	US-09-389-528-18
16	377.6	25.2	1176	4	US-09-181-827A-18
17	245.6	16.4	1588	1	US-08-706-037-24
18	245.6	16.4	1588	2	US-09-005-397-24
19	245.6	16.4	1672	1	US-08-172-331B-13
20	223	14.9	3566	3	US-08-689-421-32
21	223	14.9	3566	4	US-09-389-528-32
22	223	14.9	3566	4	US-09-181-827A-32
23	212.4	14.2	2940	3	US-08-689-421-28
24	212.4	14.2	2940	4	US-09-389-528-28
25	212.4	14.2	2940	4	US-09-181-827A-28
26	186	12.4	3327	3	US-08-689-421-26
27	186	12.4	3327	4	US-09-389-528-26

28	186	12.4	3327	4	US-09-181-827A-26	Sequence 26, Appl
29	182.8	12.2	2860	1	US-08-462-484-7	Sequence 7, Appl
30	182.8	12.2	2860	1	US-08-441-147-7	Sequence 7, Appl
31	182.8	12.2	2860	5	PCT-US95-07536-7	Sequence 7, Appl
32	182.8	12.2	2860	5	PCT-US95-07536-7	Sequence 9, Appl
33	156.2	10.4	2925	1	US-08-462-484-9	Sequence 9, Appl
34	156.2	10.4	2925	5	PCT-US95-07536-9	Sequence 9, Appl
35	112.6	7.5	2249	3	US-08-814-052-19	Sequence 19, Appl
36	112.6	7.5	2279	3	US-08-814-052-17	Sequence 17, Appl
37	112.6	7.5	2300	3	US-08-814-052-18	Sequence 18, Appl
38	109.4	7.3	2476	5	PCT-US95-06816-1	Sequence 1, Appl
39	108.8	7.3	2476	1	US-08-749-882A-1	Sequence 1, Appl
40	108.8	7.3	2476	2	US-08-539-134-1	Sequence 1, Appl
41	106.6	7.1	3102	1	US-08-462-484-5	Sequence 5, Appl
42	106.6	7.1	3102	1	US-08-441-147-5	Sequence 5, Appl
43	106.6	7.1	3102	5	PCT-US95-07536-5	Sequence 5, Appl
44	105.2	7.0	3183	2	US-08-939-218A-1	Sequence 1, Appl
45	105.2	7.0	3187	5	PCT-US95-06815-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-462-484-3
; Sequence 3, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185,010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron

Db 2044 TCACCCGCTCCGGGCGCCACTCCACATCGAGATCAGCTGCCCCGCGACCGCTTGGCCC 2103
QY 1172 CGSGTCACGCGACCCCTTCCACCTGCACGGT----- 1203
Db 2104 CGSGTCACGCGACCCCTTCCACCTGCAGGGTGATGTTCCCTGCTTCCCTTCTATC 2163
QY 1204 -----CACGCTTCGCGGTCGTCGACGCGG 1231
Db 2164 CCGAACCAGTGTCTACGTCCGTCCTATAGCACGCTTCGCGGTCGTCGACGCGG 2223
QY 1232 GGAGCACCAGTATACACTACAGCCCGATCTTCGCGACGTCGTGACGAGGCGACG 1291
Db 2224 GGAGCACCAGTATAACTACAGCCCGATCTTCGCGACGTCGTGACGAGGCGACG 2283
QY 1292 CCGCGCGGCGACACGTCAGATCCGCTTCAGACGCAACCCCGCGCTGTTCC 1351
Db 2284 CCGCGCGGCGACACGTCAGATCCGCTTCAGACGCAACCCCGCGCTGTTCC 2343
QY 1352 TCACATGCCACATCGATTTCCACCTCGACGCGGCTTCGCGATCGTTCGACGAGGACG 1411
Db 2344 TCACATGCCACATCGATTTCCACCTCGACGCGGCTTCGCGATCGTTCGACGAGGACG 2403
QY 1412 TTCGCGACGTGAAGCGCGCAACCGGTTCCGAAGCGTTCGCGACCTGTGCCGATCT 1471
Db 2404 TTCGCGACGTGAAGCGCGCAACCGGTTCCGAAGCGTTCGCGACCTGTGCCGATCT 2463
QY 1472 ACCACGGGCTGACGCGGCTAACCACTGA 1500
Db 2464 ACACGGGCTGAGGAGGCTAACCACTGA 2492

RESULT 2

US-08-441-147-3
; Sequence 3, Application US/08441147
; Patent No. 5770418
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboge, Henrik
; APPLICANT: Schneider, Palle
; APPLICANT: Aaslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5770418o No. 5770418disk of No. 5770418th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,147
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; FEATURE:
; NAME/KEY: intron
; LOCATION: 544..592
; FEATURE:
; NAME/KEY: intron
; LOCATION: 837..899
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1014..1066
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1133..1187
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1284..1342
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1752..1815
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1873..1928
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2136..2195
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(364..543, 593..661, 716..835, 900..1013,
; LOCATION: 1067..1132, 1188..1283, 1343..1498, 1554..1751,
; LOCATION: 1816..1872, 1929..2135, 2196..2489)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 662..715
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1499..1553
US-08-441-147-3
Query Match 51.5%; Score 771.8; DB 1; Length 2880;
Best Local Similarity 70.7%; Pred. No. 9.9e-164;
Matches 1463; Conservative 0; Mismatches 37; Indels 569; Gaps 10;
QY 1 GCCATCGGCGCGGTGGCGAGCCTCGTCGTCGCGAAGCCCGCTCGCGCCCGACGCGCTTC 60
Db 424 GCCATCGGCGCGGTGGCGAGCCTCGTCGTCGCGAAGCCCGCTCGCGCCCGACGCGCTTC 483
QY 61 CTTCCGGATGCCATCGTGTCAACGCGTGGTCCCTTCCCGCTCATCACCGGAAGA-- 118
Db 484 CTTCCGGATGCCATCGTGTCAACGCGTGGTCCCTTCCCGCTCATCACCGGAAGAAG 543
QY 119 -----AGGGAGACCGCTTT 131
Db 544 GTCGCGGTGTCGTCGTCCT 603
QY 132 CCAGCTCAACGTCGTCGACACCTTGACCAACACACAGCATGCTCAAGTCCAGTAGTATC-- 189
Db 604 CCAGCTCAACGTCGTCGACACCTTGACCAACACACAGCATGCTCAAGTCCAGTAGTATC 663
QY 190 -----CACTGGCA 197
Db 664 AAGTGTACGATCCGAATGTGACATCAATCGGGGCTAATTAACCGGCGACAGCACTGGCA 723
QY 198 CGGCTTCTCCAGGAGGCGACCACTGGCGACAGCGACCCCGGTCGTCAACAGCTGCC 257
Db 724 CGGCTTCTCCAGGAGGCGACCACTGGCGACAGCGACCCCGGTCGTCAACAGCTGCC 783
QY 258 TATTGCTTCGGGCGATTCATTTCTGTACACTTCCATGTGCCCGACGACGCA----- 309
Db 784 TATTGCTTCGGGCGATTCATTTCTGTACACTTCCATGTGCCCGACGACGCAAGAG 843
QY 310 -----GGAA 313
Db 844 GATTTTCTGGGTCGCCCGTGTGATGCAATGTTCTCATGTCGCGACGTGATCGACAGGGA 903

QY 314 CGTCTGGTACACAGTATCTGTCTAGCAATACTGTGACGGCTCGGAGGACCGTTG 373
Db 904 CGTTCTGGTACACAGTATCTGTCTAGCAATACTGTGACGGCTCGGAGGACCGTTG 963
QY 374 TCGTGTAGGACCCCAAGGATCCGACCGCAGCCCTACGATGTTGACAAC----- 423
Db 964 TCGTGTAGGACCCCAAGGATCCGACCGCAGCCCTACGATGTTGACAATGTAGTCCGC 1023
QY 424 -----GAGAGCAGGTCATCAC 440
Db 1024 CACGGAGTATATACACAGATCGGTTGACGTGGGGCCACAGAGAGAGCGTCATCAC 1083
QY 441 GTTGACCGACTGTGACACACCGCTGCCCGGCTCGGTCGACAGTTCCCA----- 489
Db 1084 GTTGACCGACTGTGACACACCGCTGCCCGGCTCGGTCGACAGTTCCCAAGTTCCCAAGTCCGCA 1143
QY 490 -----CTCGGCGGACGCCA 505
Db 1144 ATGGCTTAGTGTTCACAGTTCTTTTGTATGTTGCTTCGATAGCTCGGCGGACGCCA 1203
QY 506 CGCTCATCAATGGTCTTGGGGGCTCGGCTCCACTCCACCGCGCTGCTGTGTATCA 565
Db 1204 CGCTCATCAAGGCTCGGGGCGGCTCGGCTCCACTCCACCGCTGCTGTGTATCA 1263
QY 566 ACGTCCAGCAGGAAGCGC----- 585
Db 1264 ACGTCCAGCAGGAAGCGCTGAGCAATCTCTTGTATGCAATTTCAATGCTTTGTGCTG 1323
QY 586 -----TACCGCTCGGCTCGTTCGATCTCGGACCGCACTA 626
Db 1324 ACCTATCGGAACCGCAGTACCGCTCTCGTTCGATCTCGTGTGACCGCACTA 1383
QY 627 CACGTTAGCATCGACGGGCAATCTGACCGTCTGAGGTGACGCTGATCAACAGCCA 686
Db 1384 CACGTTAGCATCGACGGGCAACCTGACCGTCTGAGGTGACGCTGATCAACAGCCA 1443
QY 687 GCCTCTCCTGCTGACTATATCCAGATCTTCGCGCGGACGGCTACTCTTTGT----- 740
Db 1444 GCCTCTCCTGCTGACTATATCCAGATCTTCGCGCGACAGGCTACTCTTTGTGTAAG 1503
QY 741 -----GTTGATCGGA 751
Db 1504 TCCTGGCTGTGATGCTTCCAAAGTGGGCTCACTCATATATCTTGTGATGTAAGTGGGA 1563
QY 752 ACCAAACGGTCCGCAACTACTGGGTGCGGCAACCGCAACTTCGGAACGGTTGGGTTCG 811
Db 1564 ATCAACGGTGGCAACTACTGGGTGCGGCAACCGCAACTTCGGAACGGTTGGGTTCG 1623
QY 812 CCGGGGGGATCACTTCGCGCATCTGCGCTACCAAGGGCACCAGTCCGCGGACCACTA 871
Db 1624 CCGGGGGGATCACTTCGCGCATCTGCGCTACCAAGGGCACCAGTCCGCGGACCACTA 1683
QY 872 CGACCCAGACGCTCGGTGATCCGCTTATCGAGAGAACTTCACCCCTCGCTCGCA 931
Db 1684 CGACCCAGACGCTCGGTGATCCGCTTATCGAGAGAACTTCACCCCTCGCTCGCGCA 1743
QY 932 TGCTGT----- 938
Db 1744 TGCCAGTGTATGCTCTTTCTGATCATCTGAGTTCGCCGTCTTGACCGCATATGT 1803
QY 939 -----GCCGTGGAGCCCGACACCCCGGGGCGTGCAGACGGGCTCAACCTCGCG 987
Db 1804 GTTACTATCTAGCTTGGAGCCCGACACCCCGGGGCGTGCAGACGGGCTCAACCTCGCG 1863
QY 988 TTTACTTC----- 996
Db 1864 TTTACTTC----- 1923
QY 997 -----AAGCGACCAACTCTTTCATCAACAGCGGCTTTTCACCGCGGCGGACCGTCCCGG 1051
Db 1924 TTCAGAACGGGACCAACTCTTTCATCAACAGCGGCTTTTCACCGCGGCGGACCGTCCCGG 1983
QY 1052 TACTCTCCAGATCTGAGCGGTGGCAGACCGGACAGACCTGCTCCCTGACGCTCTG 1111

Db 1984 TACTCTCCAGATCTGAGCGGTGCGCAGACCGCAAGACCTGCTCCCGCAGGCTCTG 2043
QY 1112 TCTACCGCGTCCCGGCGCACTCCACCATCAGATCAGCTGCGCGGACCGCTTGGCC 1171
Db 2044 TCTACCGCGTCCCGGCGCACTCCACCATCAGATCAGCTGCGCGGACCGCTTGGCC 2103
QY 1172 CGGGTGACCGCAGCCCTTCCACCTGCACGGT----- 1203
Db 2104 CGGGTGACCGCAGCCCTTCCACCTGCACGGTGTATGTTCCCTGCTTCCCTTCTTATC 2163
QY 1204 -----CACGGCTTCGCGGTGCTTCGCGAGCGCG 1231
Db 2164 CCGGAACAGTGTCTAGCTCCCTCCATCTAGCAGCGCTTCGCGGTGCTTCGCGAGCGG 2223
QY 1232 GGAGCACCACTATACTACAAAGCAGCCGATCTTCGCGAGCTGCTGAGCACGGCACGC 1291
Db 2224 GGAGCACCACTATACTACAAAGCAGCCGATCTTCGCGAGCTGCTGAGCACGGCACGC 2283
QY 1292 CCGCGCGGCGGACAGCTCAGCATCCGCTTCAGAGCGGACAAACCCCGGCGCTGCTTC 1351
Db 2284 CCGCGCGGCGGACAGCTCAGCATCCGCTTCAGAGCGGACAAACCCCGGCGCTGCTTC 2343
QY 1352 TCCACTGCCACATCGACTTCCACTCGACGGGCTTCGCGATGCTTCGCGAGGACG 1411
Db 2344 TCCACTGCCACATCGACTTCCACTCGACGGGCTTCGCGATGCTTCGCGAGGACG 2403
QY 1412 TTGGGACGCTGAAGCGGCGAAACCGGTTCCGAAGGCTGCTCGAGCTGTGCCGATCT 1471
Db 2404 TTGGGACGCTGAAGCGGCGAAACCGGTTCCGAAGGCTGCTCGAGCTGTGCCGATCT 2463
QY 1472 ACGACGGGCTGAGGAGGCTTAACAGTGA 1500
Db 2464 ACGACGGGCTGAGGAGGCTTAACAGTGA 2492

RESULT 3
PCT-US95-07536-3
; Sequence 3, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07536
; FILING DATE: 15-June-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/265,534
; FILING DATE: 24-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

Qy	1052	TACTCTCAGATTCTGAGCGGTGGCAGACCGCACAGAACTGCTCCGTGCAGGCTCTG	1111
Db	1984	TACTCTCAGATTCTGAGCGGTGGCAGACCGCACAGAACTGCTCCCGCAGGCTCTG	2043
Qy	1112	TCATACCGGTCGCGGCCACTCCACATTCGAGATCACGCTGCCCGCAGACGCGCTTGCGCC	1171
Db	2044		
		TCATACCGGTCGCGGCCACTCCACATTCGAGATCACGCTGCCCGCAGACGCGCTTGCGCC	2103
Qy	1172	CGGGTGACCGCACCCTTCCACCTGCACGGT-----	1203
Db	2104	CGGGTGACCGCACCCTTCCACCTGCACGGTGTATGTTCCCTTGCCCTTCCCTTCTTATC	2163

Qy	1204	-----CAGCGCTTCGCGGTGCTTGGCAGCGCG	1231
Db	2164	CCGGAACAGTGCTACGTCGCTGCCCATCTAGCAGCGCTTCGCGGTGTTTCGACAGCGCG	2223
Qy	1232	GGAGCACGAGTATACTACAACGACCGATCTTCCGGCAGCTGTTGAGACACGGGCACGC	1291
Db	2224	GGAGCACGAGTATACTACAACGACCGATCTTCCGGCAGCTGTTGAGCACGGGCACGC	2283
Qy	1292	CCGCGCGGGCGACAACGTCACGATCCGCTTCCAGACGGAACCCCGGGCGGTGTCC	1351
Db	2284	CCGCGCGGGCGACAACGTCACGATCCGCTTCCAGACGGAACCCCGGGCGGTGTGTCC	2343
Qy	1352	TCACATGCCACATPCGACTTCCACCTCGACGCGGGGTTCCGCATCGTGTTCGACAGGACG	1411
Db	2344	TCACATGCCACATPCGACTTCCACCTCGACGCGAGGCTTCCGCATCGTGTTCGACAGGACG	2403
Qy	1412	TTGCGGACGTTGAAGCGCGGAACCCGGTTCCGAAGCGGTGTTGCGAACCTGTGCCCGATCT	1471
Db	2404	TTGCGGACGTTGAAGCGCGGAACCCGGTTCCGAAGCGGTGTTGCGAACCTGTGCCCGATCT	2463
Qy	1472	ACGACGGGCTGAGCGAGGCTAACCACTGA	1500
Db	2464	ACGACGGGCTGAGCGAGGCTAACCACTGA	2492

RESULT 4

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US-09-221-275-3
; Sequence 3, Application US/09221275
; Patent No. 6329332
; GENERAL INFORMATION:
; APPLICANT: Borneman, William S.
; APPLICANT: Bodie, Elizabeth A.
; APPLICANT: Graycar, Thomas P.
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: Pleurotosis Phenol Oxidizing Enzymes
; FILE REFERENCE: GC557
; CURRENT APPLICATION NUMBER: US/09/221,275
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cdna
US-09-221-275-3

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	Query Match	34.6%	Score 519;	DB 4;	Length 1722;
	Best Local Similarity	63.6%;	Pred. No. 2.6e-107;		
	Matches 900;	Conservative	0;	Mismatches 485;	Indels 30;
	Gaps				
Qy	92	TCCTTCCCGCTCATC	CGGGGAAGAGGAGACGGCTTCCAGCTCAACGTCGTCGACA	151	
Db	252	TTCTGGCGTTCGTTC	AAGGAACAGGGTGATAACTCCAGCTGAACGTCGTCGAATC	311	
Qy	152	CCTTGACCAACACAG	ACTGCTCAAGTCGCACCTAGTATCCACTGGCAGCGGCTCTTCTCCAGG	211	
Db	312	AAATTATCGGACAGC	ACATGTTGAAGACACCAAGTATCCATTGGCACCGGTTCTTCTCCAG	371	
Qy	212	CAGSGACCAACTGGG	CAGAGACCGCGCTTCGTCAACACAGTGCCTATTGCTTCCCGGCG	271	

[illegible]

Db	1440	GCA --- -	CGATGCGAAGCAGCAACGTCACCTATTTCGCTTCGTGACCGACAACACGAGCCCGT	1496
Qy	1346	GGTTCTCCAC	TGCCACATCGACTTCCACCTCGACGCGGGCTTCGCGATCGTGTTCCGAG	1405
Db	1497	GGTTCTCCAC	YGTATATGATGGCATCTCGAAATGGTTCGCTGTCGTTTTTCGCCG	1556
Qy	1406	AGGACCTTTC	CGGACGTGAAGCGGGGGAACCCCGTTCCGAAAGCGGTGTCGGAACCTGTGCC	1465
Db	1557	AAGACGTGAC	ATCCATTTCGGCCCC - - - - - ACCTGCCGCGTGGGACGACTGTGTGCC	1607
Qy	1466	CGATACGACG	GGCGTGACGAGGCTAACCACTGA	1500
Db	1608	CCATATATGAT	GCTTTGAGCGACAACGACAAAGGA	1642

RESULT 5

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US-08-689-421-20
; Sequence 20, Application US/08689421
; Patent No. 6008029
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberley M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Haikier, Torben P
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60080290 No. 6008029disk of No. 6008029th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,421
; FILING DATE: 9-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4554.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1170
US-08-689-421-20

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Qy	310	GGAAAGCTTCTGGTACCACAGTCATCTGTCTACGCAATACTGTGACGGGCTCGGAGGACCG	369
Db	121	GGTACTTCTGGTACCACATCCCATACGAAATCGCAATATTGTGACGGTGTTCGGTGGGGCT	180
Qy	370	TTCTGCTGTGACGATACCCCAAGGATCCGACGCGCAGCCGCTACGATGTTTGACAACGAGAC	429
Db	181	ATGTCGTGTATGACCCATGCGACCCACATCGCAACTTGTATGACATTGACAACGAGGCC	240
Qy	430	ACGCTCATCATCGTTGACCGCATGGTATACCACACCGCTGCCCGGCTCGGTCCAGAGTTCCCA	489
Db	241	ACGATCATTAACGCTCGAGACTGGTATACGTCGCCCTGC---TCCCTCTGCAAGGTCGTGT	297
Qy	490	CTCGGCGGACGCCACGCTCATCTGCTATTCATTCATTCGCTTGGCGGTCGGGCTCCCACTCCAC	549
Db	298	CCCAACCCAGATTCCACGCTTATCAACGGTATAGGGCCGATATGCTGTTGGGCCCTTACCCTA	357
Qy	550	GCCTTTCCTGTGATCAACGCTCCAGCACGCGAAAGCGCTACCGCTTCGCTCTGTTTCCGATC	609
Db	358	CCTCTCGCGGTCAATTTCTGTATAACCCGAAACCGACGATACCGGTTCCGCTTGTGTTCCCTT	417
Qy	610	TCGTGCAACCGCAACTACAGTTTACAGATTCGACATCGAGGGCACAATCTGACCGTCAATCGAG	669
Db	418	TCATGCGATCCTAATTATGATTCTCTATACGATGGGCATACCAATGACTGTTTATTGAGGTC	477
Qy	670	GACGGTATCAACGACCGAGCTCTCCCTTGTGCTGACTCTATCCAGATCTTCGCGCGCAGCGC	729
Db	478	GACGAGGTTAACGTCCAACCTCTGCTGTGCTGACTCGATCCAGATCTTCGAGGTCACGCGC	537
Qy	730	TACTCCTTTGCTGTGAATGGGAACCAACGCTGGCAACTACTTGGGTCGCGCGCAACCCG	789
Db	538	TACTCGTTCGTTCTCAACGCCAACCCGCCGCTGGCAACTACTTGGGTCGAGCAACCCG	597
Qy	790	AACCTTCGGAACGGTTGGTTTCGCGGGGGATCAACTCGGCATCTCGCTACCAAGGC	849
Db	598	AACATCGGTACTAGGGGCTTCGTGGTGAGTGCAATCTGCGATTCGCGCTATGTGGGC	657
Qy	850	GCACAGTTCGCGAGGCCACTAGACCCACAGACGACTCGGTGATCCGCTTATCGAGACG	909
Db	658	GCTTCCAATACAGACGCCACTACCAACCAACTCCTTTTCAGCAACCCCTCTCCTTGAGACC	717
Qy	910	AACCTTGACCCCTCGCTCCGATCGCTGTGCTGGCAGCCGACACCCGGGGGCTGCAC	969
Db	718	AATCTCAACCCCTTGACCAACCCCTGCTGCTGTGCTTACCCGAGTGGGGTCGAC	777
Qy	970	AAGCGCTCAACCT-----CGGGTTTAACCTTCAACGGCACCACCTTCTCATCAACAAC	1023
Db	778	GTGCGATCAACCTTAACAGGTTATTCGATTTTCAGTAGTCTCACTTCTCCGTTAACGGA	837
Qy	1024	CGCACTTTCAGCGGGGACCGTCCCGGTACTCTCCAGATTCGTAGGGGTCGCGACAC	1083
Db	838	GCCACTTTCATCAACGCGCGCTGCTTGTGTTTCAGATCATGAGCGGTCGACAGACT	897
Qy	1084	GCACAAGACCTGCTCCTCGAGGCTCTGCTTACCGCTCCCGGCCACTTCCACCATCGAG	1143
Db	898	GCCACGAGCTTCTTCCCTCGGTTCCGTTCTAGTCTCTTCCCGTAACAAGTCAATCGAG	957
Qy	1144	ATCAGCTGCGCGACCGGCTTTGGCCCGGGTGACCGCAACCCCTTCCACCTCGACCGT	1203
Db	958	CTTTTCTAGCTGGAGC-----TCCACTGGCAGTCCCAATCCCTTCCATCTCCACGGT	1011
Qy	1204	CACGCTTCCGGTCTTCCAGCGGGGGACCAACGATATACTACAACGACCCGATC	1263
Db	1012	CACGAATTTGCTGTGTGAGAGCGGGGAGTTTCGACTTACAACCTTCGCAACCCCGGTA	1071
Qy	1264	TTCCGCGACGCTGTGAGACAGCGGACCGCCGCGGGGCGACAACGTCACGATCCGCTTC	1323
Db	1072	GCGAGGNTGCTGTAGTCCGG-----TGTTGCTGGTGACAGCTCACCATTCGATTC	1125
Qy	1324	CAGACGGACAACCCCGGGCGGTGTTCTTCCACTGCCACATCGAC	1368
Db	1126	CGTACCGAATAACCTGGACCATGGATTCTTCCATTGCCATATTCGAC	1170


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; TITLE OF INVENTION: Acids Encoding Same
; FILE REFERENCE: 4534.200-US
; CURRENT APPLICATION NUMBER: US/09/181.827A
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/002.800
; PRIOR FILING DATE: 1995-08-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Coprinus cinereus
; US-09-181-827A-20

Query Match          31.5%; Score 472.6; DB 4; Length 1170;
Best Local Similarity 65.0%; Pred. No. 5.5e-97;
Matches 770; Conservative 0; Mismatches 394; Indels 21; Gaps 4;

QY 190 CACTGGCAGCGCTCTTCCAGGAGGACCACTGGGCAGACGAGCCGCGTTCGTCAAC 249
Db 1 CACTGGCAGCGCATGTTCAAAGGGGACTGCCTGGGCTGATGCTCGTGGCGTCAAC 60

QY 250 CACTGGCCCTATTGCTCCGGGCAATTCATTTCTGTACGACTTCCATGTGCCCGACGAGCA 309
Db 61 CANTGCCCTATTTCGCCAGGGCAATTCGTTCTGTACAAAGTTCCAGGCTCTTAACCAAGCC 120

QY 310 GGAACGCTTCGTGACACAGCTATCTGTCTACGCAATCTGTGACGGGCTCGGAGGACCG 369
Db 121 GGTACTTTCTGTGACCACTCCCATCAGCAATTCGCAATATTTGACGGTTTTCGCTGGGGCT 180

QY 370 TTGCTGCTGTACGACCCCAAGGATCCGACGCGCCAGCGCTACGATGTTGACACGAGAGC 429
Db 181 ATGCTGTATATGACCGCATTCGACCCACATCGCAACTTGTATGACATTTGACAAACGAGCC 240

QY 430 ACGGCTATCATCGTTGACGAGTGTGACACACGCGCTGCCGGCTCGGTCCCGAGTTCCCA 489
Db 241 ACGATCATTAAGCTCGAGACTGATATCAGTCCCTGC---TCCCTTCGAGGTCCTGTT 297

QY 490 CTGCGGCGGACGCGAGCTCAATGTCCTTGGGGGCTGGGCGTCCGCTCCATCCCAAGCGC 549
Db 298 CCCAGCCAGATTCCACGCTTATCAACGGTAAGGGCGGCTATGCTGGTGGCCCTACCGTA 357

QY 550 GCGCTTGTCTGTATCAACGTCACGACGCGGAAAGCGTACCGCTTCGCTCTCGTTTCGATC 609
Db 358 CTTCTCGCGTCAATTTCTGTAACCCGGAACCGAGATACCGGTTCCCGCTTGTTCCTTT 417

QY 610 TCTGCGACCCGCACTACAGTTTACGATCGACGGGACAACTCTGACCGCTCATCGAGGTC 669
Db 418 TCATGCGATCCTAATATGATTTCTCTATCGATGGGATACCATGACTGTTATGAGGTC 477

QY 670 GAGGCTATCAACAGCCAGCCTCTCTTGTGCTACTATATCAGATCTTTCGCGGCGCAGCGC 729
Db 478 GACGGAGTTAACGTCCAACTCTCTGTTGCTGACTCGATCCAGATCTTCGCGAGGTCAGCGC 537

QY 730 TACTCTCTTGTGTTGAATGGAACCAACGCTGCGCAACTACTGCGTTCGCGCGAACCAG 789
Db 538 TACTGTTGTTCTCAACGCCAACCCCGCCGCTCGGAACCTACTGCGGTGCGAGCAACCC 597

QY 790 AACTTCGGAACGGTTGGTTGCGGGGGGATCAACTCCGCCATCTCGCTACCAAGGC 849
Db 598 AACATCGGTACTACGGCTTCGTCGGTGGAGTCAATCTCGATTCGCGATATGTGGGC 657

QY 850 GCACCACTGCGGAGCCACTAGACCCAGACAGCTCGGTGATTCGCGTTCATCGAGAGC 909
Db 658 GCCTCCAATACAGACCCCACTACCAACCAACTCTTTCAGCAACCCCTCTCTCTTGAGACC 717

QY 910 AACTTGACCCCTCGCTCGCATGCTGCTGCTGGAGCCGACACCCGCGGCGCTCGAC 969
Db 718 AATCTCCACCCCTTGACCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777

QY 970 AAGCGCTCAACCT-----CGCGTTTAACTTCAACGGCACCACCACTTCTTCATCAACAC 1023
Db 778 GTCGCGATCAACCTTAACAGGATTTTCGATTTTCAGTAGTCTCACTTCTCTCGTTAAGCA 837
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QY 1024 GCACATTTCACGCGCGGACCGCTCCCGGTACTCTCCAGATTCTGAGCGGTGCGAGACC 1083
Db 838 GCCACTTTCATCAACCGCCGCTCCCTGTCTTCTCAGATCATGAGCGGTGCGACAGACT 897
QY 1084 GCACAAGACCTGCTCCCTCGAGGCTCTGTACCCGCTCCCGGCCCACTCCACCATCGAG 1143
Db 898 GCCAGCAGCTTCTCCCTCGGTTCCGTTAGCTCTCCCGGTACCAAGTCAATCGAG 957
QY 1144 ATCAGCTGCCGCGGACCGCTTGGGCGCGGCGTGCACCGCACCCCTTCCACCTGCGAGGT 1203
Db 958 CTTTCTATGCTTGAGGC-----TCCACTGGCAGTCCCATCCCTTCCATCTCCACGGT 1011
QY 1204 CAGCCCTTCGCGGTTCGTCAGCGGGGAGCACCACGCTATTAACATAACAGCCGATC 1263
Db 1012 CAGCAATTTCTGCTGGTGAGAGCGCGGGAGTTGCACTTCACTTTCGCGAACCCGTA 1071
QY 1264 TTCGGGACGCTGTCGAGCAGCGGACGCCCGCGCGGCGGCGACAACTGACAGTCCGCTTC 1323
Db 1072 CGCAGGATGCTGCTGAGTGCCG-----TGTTGCTGTCGACAACTGCACTTCGATTC 1125
QY 1324 CAGACGACAAACCCGCGCGCTGCTTCTCCACTGCCACATCGAC 1368
Db 1126 CGTACCGATAACCTGGACCATGATTCCTCCATTCGCAATATCGAC 1170
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RESULT 8
US-08-462-484-1
; Sequence 1, Application US/08462484
; Patent No. 5667531
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Xu, Feng
; APPLICANT: Dalboe, Henrik
; APPLICANT: Schneider, Pallo
; APPLICANT: Aslyng, Dorrit A.
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5667531o No. 5667531disk of No. 5667531th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,484
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,147
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowrey, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
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Query Match	30.2%;	Score 452.8;	DB 1;	Length 2418;
Best Local Similarity	69.0%;	Pred. No. 1.7e-92;		
Matches 708;	Conservative 0;	Mismatches 207;	Indels 111;	Gaps 2;

QY	586	TACCGCTTCGCTCGCTTTTCGATCTCGTGGACCCGAACTACAGCTTCAGCATCGACGGG	645
Db	1198	TACCGTTTCGCGCTGGTCTCCCTCGTGGACCCCACTACAGCTTCAGCATCGATGGT	1257
QY	646	CACAATCTGACCGTCATCGAGGTGCAGGGTATCAACAGCCAGCCCTCTCCTTGTGCAGCTCT	705
Db	1258	CACAACATGAGGATCATCGAGACCGACTCAATCAACAGCGCGCCCTCGTCTGCAGCTCC	1317
QY	706	ATCCAGATCTTTCGCGGGCAGCGCTACTCTCTTTGTGTGA	745
Db	1318	ATTCAAGATCTTCGCGCCACGCTACTCTCTCGTGGTAACTTCGATTCATCCTCTCAACG	1377
QY	746	-----ATGCGACCAACCGTCGGCAAC	768
Db	1378	TTGTGCTGCTTTAGTGATCTGATGTCATGTCAGGCGCAACACGAGCGCTGCAGAAC	1437
QY	769	TACTGGGTCCGCGGGAACCCGAACTTCGGAAAGGTTCGGTTCGCGGGGGATCAACATCC	828
Db	1438	TACTGGATTCCGCGCAACCCGAACTTCGGTAACTCGTGGTTCACGGCGGATTAACTCG	1497
QY	829	GCAATCTGCGCTACCAAGGGCGACAGTCCGCGAGCCCATAGACCCAGCAGCTCG	888
Db	1498	GCTATCTCCGCTACGATGGTCCGCTCGCGTGGAGCCACCAACGCAACACGCTCG	1557
QY	889	GTGATCCGCTTATTCGAGACGAATTCACCCCTCGCTCGCATGCGCT	938
Db	1558	ACTCGCGGCTCAACGAGGTCAACTGCACCCGCTGGTTACACCGCTGTGGTATGTAAT	1617
QY	939	-----GCGTGGAGCCCGGACA	954
Db	1618	ATTTCGGTGAATGAATACATTTGTGTGACTCGACCCCAACAGCGCTGGCTCGCCGCTC	1677
QY	955	CCCGGGGCGTCGACAGGCGCTCAACTCGCTTTTAACTTCAACGGCACCACTCTCTC	1014
Db	1678	GCTGGTGTGTCAGCTTGGCCATCAAGATGCGTTTCAACTTCAACGGCACCACTCTCTC	1737
QY	1015	ATCAACACGCGACTTTTCAGCCCGCCAGCGTCCCGGTACTCTCCAGATTTCTGAGCGGT	1074

US-08-441-147-1
: Sequence 1, Application US/08441147
: Patent No. 5770418
: GENERAL INFORMATION:
: APPLICANT: Yaver, Debbie Sue
: APPLICANT: Xu, Peng
: APPLICANT: Dalboge, Henrik
: APPLICANT: Schneider, Falie
: APPLICANT: Aaslyng, Dorrit A.
: TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
: TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 5770418o No. 5770418disk of No. 5770418th America, Inc.
: STREET: 405 Lexington Avenue, Suite 6400
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/441.147
: FILING DATE: 15-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lowney, Karen A.
: REGISTRATION NUMBER: 31,274
: REFERENCE/DOCKET NUMBER: 4185.010-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 867 0123
: TELEFAX: 212 878 9655
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:

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; LENGTH: 2418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Polyporus pinsitus
; FEATURE:
; NAME/KEY: intron
; LOCATION: 414..464
; FEATURE:
; NAME/KEY: intron
; LOCATION: 534..589
; FEATURE:
; NAME/KEY: intron
; LOCATION: 710..764
; FEATURE:
; NAME/KEY: intron
; LOCATION: 879..934
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1001..1050
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1147..1197
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1354..1410
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1609..1662
; NAME/KEY: CDS
; LOCATION: join (413..465, 533..590, 709..765, 878..935,
; LOCATION: 1000..1051, 1146..1198, 1353..1411, 1608..1663)
; US-08-441-147-1

Query Match
Best Local Similarity 30.2%; Score 452.8; DB 1; Length 2418;
Matches 708; Conservative 0; Mismatches 207; Indels 111; Gaps 2;

QY 586 TACCGCTTCGCTCGCTTCGATCTGTCGACCGCACTACAGTTTCAGCATCGAGCGG 645
Db 1198 TACCGTTCCGCTGGTGTCCCTGTGTCGACCCCACTACAGTTTCAGCATCGATG 1257
QY 646 CACAATCTGACCGTCAATCGAGGTCGAGGATCAACAGCCAGGCTCTCTGTGACTCT 705
Db 1258 CACAATGACGATCATCGAGACGACTCAATCAACAGCGGCCCTCTGTGACTCTC 1317
QY 706 ATCAGATCTTCGCGCGGACGCTACTCTCTTTGTGTGA----- 745
Db 1318 ATTCAGATCTTCGCGCGGACGCTACTCTCTGTGTAAGTTCGATTCATCTCTAAG 1377
QY 746 -----ATCGCAACCAACGCTCGCAAC 768
Db 1378 TTGGTCGCTGTAGTATCTATGTCATGTAGCTGAGCCCAACAGCGCTCGACAA 1437
QY 769 TACTGGTCCGCGCAACCGAATTCGGAAACGTTGGTTCCGCGGGGGATCAACTCC 828
Db 1438 TACTGGATTCCGCGCAACCGAATTCGGTAACGTCGGTTTACCGCGCGCATTAAC 1497
QY 829 GCCATCTGCGTACCAAGCGGACCAAGTCGCGGAGCCCACTAGGACCCAGACGTCG 888
Db 1498 GCATCTCCGCTACGATGTGGCGGTGCGGTGAGCCCAACAGCAACCAACGTCG 1557
QY 889 GTGATCCCGCTTATCGAGACGAATTCACCCCTCTCTCGCATGCTGT----- 938
Db 1558 ACTGCGCGCTCAACGAGGTCAACCTGACCCGCTGTGTACACCGCTGTGGTATGA 1617
QY 939 -----GCGTGCAGCCCGACA 954
Db 1618 ATTGTGGTAATGTAATACATTGTTGTGACCTCGACCCCAACAGCGCTGCGCGGTC 1677
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QY 955 CCGGGGCGCTCGAAGCGCTCAACCTCGCGTTTAACTTCAACGCGCAACTTCTTC 1014
Db 1678 GTGGTGTGTGACCTGGCCATCAACATGCGTTCAACCTCAACGCGCAACTTCTTC 1737
QY 1015 ATCAACAACGCGACTTTTCAGCGCGCGACCGTCCCGTACTCTCTCCAGATTTCTGAGCGGT 1074
Db 1738 ATCAACGCGCGCTTTTCAGCGCGCGACCGTCTCTCTGCTCCAGATCATCAGCGGC 1797
QY 1075 GCGCAGACCGCACAGACCTGCTCCCTGACAGGCTCTGTCTACCGGCTCCGCGGCCACTCC 1134
Db 1798 GCGCAGAACGCGGAGGACCTCTCTGCGGTAGCGCTACTGCTTCCCTCGAACGCC 1857
QY 1135 ACCATCGAGATCAACGCTGCGCGGACCGCTTTGGCCCGCGGTGACGCGACCCCTTCCAC 1194
Db 1858 GACATCGAGATCTCTTCCCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1917
QY 1195 CTGACGCTTCAGCGCTTCGCGGTGCTGTCGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 1254
Db 1918 TTGCACGCGCGCTTCGCGGTGCTGTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1977
QY 1255 GACCCGATCTTCGCGGAGCTGTCGTCGAGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1314
Db 1978 AACCCCATCTTCGCGGACGCTGTCGACGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2037
QY 1315 ATCCGCTTCCAGCGGACAAACCCCGCGCGCTGTCGACGACGCGGCGCGCGCGCGCGCGCGCGCG 1374
Db 2038 ATCCGCTTCCGCGACCGACAAACCCCGCGCGCTGTCGACGACGCGCGCGCGCGCGCGCGCGCG 2097
QY 1375 CTGACGCGCGGCTTCGCGATGCTGTCGAGAGGACGCTTCGCGACGTTGCGGACGTGAAGCGCGCAAC 1434
Db 2098 CTGAGCGCGCTTCGCGGTGCTGTCGAGGAGACATCCCGACGTCGCGCGCGCGCGCGCGCGCG 2157
QY 1435 CCGGTTCCGAGGCGTGTGCGACCTGTCGCGCGCTGTCGCGCGCTGTCGCGCGCTGTCGCGCGCT 1494
Db 2158 CCGTCCCGCGGCTGTCGCGCGCTGTCGCGCGCTGTCGCGCGCTGTCGCGCGCTGTCGCGCGCT 2217
QY 1495 CAGTGA 1500
Db 2218 CAGTAA 2223

RESULT 10
PCT-US95-07536-1
; Sequence 1, Application PC/TUS9507536
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07536
; FILING DATE: 15-June-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/265,534
; FILING DATE: 24-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4185.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 878 9655
```



```

Qy 970 AAGCGGTC AACCTCGCGTTTAACTTTCAACGGCAC-----CAACTTCTTCAATCAACAC 1023
   || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 778 GTCCGCTCAACCTGGGATATCTTTGTTGCGAGCTCTCAATCCTCAAGTTCACTGTCAACGGT 837
   || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1024 GCGACTTTCAGCGCGCGGACCGTCCCGGTACTCTCTCCAGATTCTGAGCGGTGCGCAGACC 108
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 838 GCTACCTTCGATGACCAACCGCTTTCGGTCTCTCTCCAGATTCTGAGCGGTGCGCAGATACC 897
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1084 GCACAAGACCTTGCTCCCTCGAGGCTCTGTCTACCCGCTCCCGGCGCCACTTCCACCACTCGAG 114
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 898 GCCTCAVCTCTCTCCCTCTGCGCAGGCTGTACACTTCTCCCTTAACAAGTCAATTCAG 957
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1144 ATCAGCTGCGCGGACCGCTTGGCGCCCGGGTGACCGCAGCCCTTTCACCTGCAACGGT 1203
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 958 CTCACTATTCCCGGTGGTGAT-----CGGTGCTCTCACCCCATCATCTTTCACGCGC 1011
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1204 CACGCCCTCGCGGTCTCCAGCGTCCAGCGGGGAGCACCACGTATATACTACAAAGACCCGATC 126
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1012 CATACCTTCAAGTTGTCTCGTACCGCAGCAGCTCGACTTACACTTCTGTAATCCCGTT 1071
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1264 TTCCGCGACGTGTGAGCAGCGCACGCCCGCGCGGGCGAGCAAGCTCACGATCCGCTTC 1322
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1072 GAGCGCATGTGTCTCAACGTTCG-----TCAAGTGTGGCGACAATGTCAACATTCGATTC 1129
   || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1324 CAGACGACAAACCGCGCGGTCTCTCCACTGCG 1359
   || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 1126 GTCACTGATAATGCTGGTCTGGATTCCTCACTGC 1161
   || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

RESULT 12
US-09-389-528-22
: Sequence 22, Application US/09389528
: Patent No. 6207430
: GENERAL INFORMATION:
: APPLICANT: Yaver, Debbie S.
: APPLICANT: Brown, Kimberley M.
: APPLICANT: Kauppinen, Sakari
: APPLICANT: Halkier, Torben P
: TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
: TITLE OF INVENTION: PURIFIED SAME
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6207430 No. 6207430disk of No. 6207430disk of No. 6207430th America, I
: STREET: 405 Lexington Avenue, 64th Floor
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/389,528
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/689,421
: FILING DATE: 9-AUG-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Harrington, James J.
: REGISTRATION NUMBER: 38,711
: REFERENCE/DOCKET NUMBER: 4554.204-WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1161 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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598 AACAGGTCGAAACGGACTTGTGGTACCTTCGCCAACGGTGTCAACTCGGCCATCCTT 657
838 CGCTACCAAGCGCCACCACTGCGGAGCCCACTAGGACCCAGACGCTCGGTGATCCCG 897
658 CGCTATCGCGCGCTGCGCAACGCTGATCAACACCTCCGCAACCCCAACCCGCGCCAA 717
898 CTTATCGAGAGAACTTGCACCCCTCGCTCGCATGCTGTGCTGGCGAGCCGACACCC 957
718 CTCAGGAAGCGGACCTCCATGCTCTCATCGACCCGCTGTCCGGTATCCCACTCCG 777
958 GGGGCGCTCGACAGGCGCTCAACTCGCGTTTAACTTCAACGGGACCAACTCTTTCATC 1017
778 GCGCTGCAGAGCTCAACCTCCGATTCCAATTGGGCTTTCAGGCGGCTCGATTACAGATT 837
1018 AACACGCGACTTTCACGCGCGGACCGTCCGGGTACTCTCCAGATTCTGAGCGGTGCG 1077
838 AACGGAACCGGATAGGAGAGTCCAAAGCTTCTTACGCTTTCAGATTATGAGTGGTCCG 897
1078 CAGACCGCACAGAGCTCTCCCTGCGAGGCTCTGTCTACCGGCTCCCGGCCACTCCACC 1137
898 CAGAGTGGAAAGCACTTCTCCCTGCTGATCGGTGTATGATTCCC-----CAGGAAC 951
1138 ATCGAGATCAGTCGCCGCGACCGCTTGGCGCGGGGTGCGACCGACCCCTTCCACCTG 1197
952 CAAGTTGTTGAGCTTGTGTTCTCTGCTGCTGATCGGTGTATGATTCCC-----CAGGAAC 1011
1198 CACGCTCAGCGCTTCGCGGTGCTTCGCGAGCGGGGAGCAGCAGCTATAACTACACGAC 1257
1012 CACGCTATGCGTTCAGTGTCTGTCAGGAGTGCAGGACGAGCAGCAGCTTGTCAAC 1071
1258 CCGATCTTCCGCGAGCTGCTGAGCAGCGGCGACGCGCGCGGCGGCGAGCAGCTCAGCATC 1317
1072 CCGGTCAGCGCGATGTTGTTAGTCTGG-----TGTTACTGGAGAGGATACCAATT 1125
1318 CGCTTCAGAGCGCAACCCCGGCGGCTGTTCTTCCACTGCGCATCGA 1367
1126 CGATTGCTCACCGATAACCGAGCGCGGTGTTCTTCCACTGCCACATTGA 1175
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RESULT 15

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US-09-389-528-18
; Sequence 18, Application US/09389528
; Patent No. 6207430
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie S.
; APPLICANT: Brown, Kimberley M.
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Halkier, Torben P
; TITLE OF INVENTION: PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6207430o No. 6207430disk of No. 6207430th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,528
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,421
; FILING DATE: 9-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
```

```

; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4554.204-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1176
US-09-389-528-18

Query Match 25.2%; Score 377.6; DB 4; Length 1176;
Best Local Similarity 60.0%; Pred. No. 9.2e-76;
Matches 714; Conservative 0; Mismatches 449; Indels 27; Gaps 4;

Qy 190 CACTGGCAGCGCTTCTCCAGGCGAGGCACCACTGGGCGAGGACCGCGTTCGTCACAC 249
Db 1 CATTGGCAGCGTCTCTCCAAAGGAGGACCAACTGGGCTGATGGTGCAGATGGTGTCAAC 60
Qy 250 CAGTGCCCTATTGCTTCGGGCAATTCATTCTGTACGACTTCCATGTGCCGACCAAGCA 309
Db 61 CAGTGCCGATCTCTCCAGGCCATGCTTCTCTACAGTTCACTCCAGCTGGCCACGCT 120
Qy 310 GGAAGTTTCTGGTACCACAGTCACTGTCTACGCAATACTGTGACGGGCTGCGAGGACG 369
Db 121 GGTACTTTCTGGTACCATTCACATTTGGCACCCCAATACTGCGATGGTCTCGTGGTCCA 180
Qy 370 TTCGTCGTGACGACCCCAAGGATCCGACGCGCCAGCCCTAGGATGTTGACAAACAGAGC 429
Db 191 ATGGTCATTACGAGCAGACATGACCCACAGCTGCGCTCTACGAGAGATGACGAGAAC 240
Qy 430 ACGGTATACGTTGACCGACTGTTACACACCGCTGCCCGGCTCGGTCCCAAGTTCACA 489
Db 241 ACCATCATTAACCTCGCGGATTGGTACCATATCCCGCTCCCTCCATTC---AGGGTGT 297
Qy 490 CTCGCGCGGAGCGCACCTCATCAATGTTTGGCGGTGCGGCTCCACTCCCAACCGCC 549
Db 298 GCCAGCTGACGCTACGCTCATCAACGTTAGGTGCTAGTGGGCGGCGGCGGCGGCT 357
Qy 550 GCGTTTGTGTGATCAACGTCACGTCACGACGAAAGCGCTACCGTTCGCTCTCGTTTCGATC 609
Db 358 GAGCTTTGATCGTCAATGTCGAGCAAGGAAGAGTACCGAATCGTTTGTATCTCGCTG 417
Qy 610 TCGTGGACCGGAACTACAGTTTACGATCGAGGCGACAACTGACCGTCAATCGAGGTC 669
Db 418 TCCTCGGACCCCACTGGCAGTTCTCCATTGACGGACATGAGTTGACGATCATTTGAAGTC 477
Qy 670 GACGGTATCAACAGCCAGCTCTCTTCTCGACTCTATCCAGATCTTCCGCGGCGAGCGC 729
Db 478 GATGTCAGCTTACGAGCGCGCATACGGTTGATGCTCTCCAGATCTTCTACTGGTCAAGG 537
Qy 730 TACTCTTTTGTGTTGAATGCGAACAACAAAGGTCGCGCAACTACTTGGGTCCGCGCAACCG 789
Db 538 TACTCTTTGTTCTCGAGCGCAACAGCGGCTGGGACAACTACTGATCGGTCTCAACCC 597
Qy 790 AACTTCGGA-----ACGGTTGGTTTCGCGGGGGGATCAACTTCGCCCATCTCGT 837
Db 598 AACAGGTCGAAACGGACTTGTGTGTTACCTTCGTCACCGAGGTTGTCACCTCGGCTT 657
Qy 838 CGCTACCAAGGCGCACAGTGCAGGCGCCCACTAGACCCAGACGACGCTCGGTGATCCCG 897
Db 658 CGCTATGCGGCGCTGCGCAACGCTGATCCAAACCACTCCGCAACCCCAACCCGCGCCAA 717
Qy 898 CTTATCGAGAGAACTTGCACCCCTCGCTCGCATGCTGCTGCTGGAGCGCGGCGGACACCC 957
Db 718 CTCAGAGAGCGGACTCTCATCTCTCATCGACCCGCTGCTCCCGGTATCCCACTCCG 777
```

```
QY 958 GGGGGGCTGCACAAAGCGCTCAACCTGCGCTTTAACTTCAACGGCACCAACTTCTTCAATC 1017
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 778 GGGGCTGCAGACGTCAACCTCCGATTCGAATTGGGCTTCAAGCGGTCGATTACAGATT 837
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1018 AACACGCGACTTTCAGCGCGCGACCGTCCCGGTACTCCTCCAGATTCTGAGCGGTGCG 1077
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 AACGGAACCGCATACGAGAGTCCAAGCGTTCCTACGCTCTTGAGATTATGAGTGGTGG 897
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1078 CAGACGCGCACAAAGACCTGCTCCCTGAGGCTCTGTCTACCCGCTCCCGGCCACTCCACC 1137
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 898 CAGAGTGCAGAACGACTTGCTCCCTGCTGGATCGGTGTATGAGTTGCC-----CAGGAAC 951
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1138 ATCGAGATCACGCTGCCCGGACCGGCTTGGCCCGGGTGCCACGACCCCTTCCACCTG 1197
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 952 CAAGTTGTTGAGCTTGTGTCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1198 CACGGTCACGCTTCGCGGTCGTTGCGAGCGCGGGGAGCACACGTATATACTACAAGAC 1257
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1012 CACGGTCATGCGTTCAGTGTGCTCAGGAGTGCAGGAGTGAGGAGCAGCAGCAGCAGCAGCAG 1071
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1258 CCGATCTTCGGCAGCTGCTGTGAGCAGCGGACCGCCCGCGCGGCGGACACAGTCACGATC 1317
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1072 CCGGTCAAGCGCGATGTTGTTAGTCTTG-----TGTTACTGGAGACGAAGTTACCAT 1125
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1318 CGCTTCCAGACGACAAACCCCGCGGCTGTTCTCCTCAGTCGACATCGA 1367
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1126 CGATTCGTACCGATAAACCAGCGGTTGTTCTTCCACTGCCACATTTGA 1175
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: December 14, 2002, 05:21:02
Job time : 103 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2002, 08:22:47 ; Search time 45 Seconds
(without alignments)
1066.024 Million cell updates/sec

Title: US-09-786-960-2
Perfect score: 2669
Sequence: 1 AIGPVASLVWANAPVSPDGF.....VPKAWSLCPIYDGLSEANQ 499

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	2243	84.0	520	2	A35883	laccase (EC 1.10.3
2	2238	83.9	520	2	B35883	ligninolytic pheno
3	1917.5	71.8	527	2	JC5357	laccase (EC 1.10.3
4	1882.5	70.5	520	2	S59533	laccase (EC 1.10.3
5	1871.5	70.1	520	2	JC5356	laccase (EC 1.10.3
6	1772	66.4	512	2	JC5355	laccase (EC 1.10.3
7	1743.5	65.3	529	2	S49120	laccase (EC 1.10.3
8	1743.5	65.3	533	2	S62371	laccase (EC 1.10.3
9	1716	64.3	548	2	S18746	laccase (EC 1.10.3
10	1175.5	44.0	529	2	S68120	laccase (EC 1.10.3
11	1000	37.5	599	2	S68118	laccase (EC 1.10.3
12	930.5	34.9	572	2	S68119	laccase (EC 1.10.3
13	901	33.8	576	2	S68117	laccase (EC 1.10.3
14	622.5	23.3	621	2	S72493	laccase (EC 1.10.3
15	608	22.8	624	2	A36962	laccase (EC 1.10.3
16	601.5	22.5	619	1	KSNCLO	laccase (EC 1.10.3
17	600.5	22.5	619	1	KSNCLT	laccase (EC 1.10.3
18	599	22.4	636	2	A5428	ferroxidase precu
19	597.5	22.4	622	2	S5214	probable membrane
20	574.5	21.5	582	2	T05020	L-ascorbate oxidas
21	567	21.2	553	2	T45959	laccase-like prote
22	566	20.8	555	2	T48347	laccase-like prote
23	556	20.8	622	2	S62580	probable multicopp
24	538.5	20.2	557	2	JC5229	laccase (EC 1.10.3
25	536.5	20.1	587	1	KSVAO	L-ascorbate oxidas
26	535.5	20.1	567	2	T44928	L-ascorbate oxidas
27	530.5	19.9	578	2	S66353	L-ascorbate oxidas
28	530	19.9	554	2	T01240	laccase (EC 1.10.3
29	524.5	19.7	570	2	T00579	probable laccase [

ALIGNMENTS

RESULT 1

A35883

laccase (EC 1.10.3.2) A - white-rot fungus (Trametes versicolor)

N:Alternate names: ligninolytic phenoloxidase 1 precursor

C:Species: Trametes versicolor (white-rot fungus)

C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 19-May-2000

C:Accession: A35883; S59526

R:Kojima, Y.; Tsukuda, Y.; Kawai, Y.; Tsukamoto, A.; Sugiyama, J.; Sakano, M.; Kita,

J. Biol. Chem. 265, 15224-15230, 1990

A:Title: Cloning, sequence analysis, and expression of ligninolytic phenoloxidase gen

A:Reference number: A35883; MUID:90368706; PMID:2394718

A:Accession: A35883

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-520 <KOJ>

A:Cross-references: GB:M60560; GB:J05562; NID:g167464; PIDN:AAA33103.1; PID:g167465

R:Joensson, L.; Sjoestroem, K.; Haegstroem, I.; Nyman, P.O.

Biochim. Biophys. Acta 1251, 210-215, 1995

A:Title: Characterization of a laccase gene from the white-rot fungus Trametes versic

A:Reference number: S59526; MUID:95399443; PMID:7669813

A:Accession: S59526

A>Status: preliminary

A:Molecule type: protein

A:Residues: 351-360 <JOE>

C:Superfamily: laccase

C:Keywords: oxidoreductase

Query Match 84.0%; Score 2243; DB 2; Length 520;
Best Local Similarity 81.8%; Pred. No. 1.6e-157;
Matches 408; Conservative 35; Mismatches 56; Indels 0; Gaps 0;

QY	1	AIGPVASLVWANAPVSPDGF	LRDAIVVGVVPSPLITGKGRFQNLNVDTLTHNSMLKS	60
DB	22	AIQPTADLLTISNAEVSFDF	GFARQAVVNVNTPGFLVAGNKGDRFQNLNLTHTMLKS	81
QY	61	TSIHWGFTQAGPNWADGPAFV	NQCPIASGHSFLYDFHVPDQAGTFWYHSHLSTQYCDGL	120
DB	82	TSIHWGFTQKGTNWADGPAFV	NQCPISSGHSFLYDFQVPDQAGTFWYHSHLSTQYCDGL	141
QY	121	RGFFVYDDPKDPHASRYDND	NESTVTLTDWYHTAARLGRPRFPLGADATLNGLSAST	180
DB	142	RGFFVYDDPKDPHASRYDND	DDTVTTLADWYHTAARLGRPRFPLGADATLNGLSRSPST	201
QY	181	PTAALAVINVHGKRYRFRFLV	SLTSCDPNTFTSDGNHNLTVIEVDGINSQPLLVDSIQIFA	240
DB	202	TAADLAVINVTKGRYRFRFLV	SLSCDPNHTFTSIDGDLTIEVDGINSQPLLVDSIQIFA	261
QY	241	AQRYSVLNNQTVGNVWRANP	NFTCTGVFAGGINSAILRYQCAPVAEPTTTQTSVIPL	300
DB	262	AQRYSVLNNQTVGNVWRANP	NFTCTGVFAGGINSAILRYQCAPVAEPTTTQTSVIPL	321
QY	301	IETNLHPLARMPVPGSPTPG	CVDKALNLPFNFGTNNFTTPTTPTVPLQLLSGAQ	360

Db 322 NEVDLHPLATMAVPGSVAGVDTAIINMAFNGTNEFFINGASFVPTVPVLLQIISGAQ 381
Qy 361 TAQDLLPAGSVYPLPAHSTIETITLPATALAPGAPHPHLLHGHAFVAVRSAGSTTYNDP 420
Db 382 NAQDLLPSGSVYSLPSNADIEISFPATAAAGAPHPHLLHGHAFVAVRSAGSTTYNDP 441
Qy 421 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIVFAEDVADVKAANPV 480
Db 442 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIVFAEDVADVKAANPV 501
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 502 PKAWSDLCPYDGLDNDQ 520

RESULT 2

B35883
ligninolytic phenoloxidase (EC 1.10.1.1) 2 precursor - white-rot fungus (Trametes versicolor)
C:Species: Trametes versicolor (white-rot fungus)
C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 19-May-2000
R:Kojima, Y.; Tsukuda, Y.; Kawai, Y.; Tsukamoto, A.; Sugiyama, J.; Sakano, M.; Kita, Y.
J. Biol. Chem. 265, 15224-15230, 1990
A:Title: Cloning, sequence analysis, and expression of ligninolytic phenoloxidase genes
A:Reference number: A35883; MUID:90368706; PMID:2394718
A:Accession: B35883
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-520 <KOJ>
A:Cross-references: GB:J05562
C:Superfamily: laccase
C:Keywords: Oxidoreductase

Query Match 83.98; Score 2238; DB 2; Length 520;

Best Local Similarity 81.68; Pred. No. 3.8e-157; Indels 0; Gaps 0;
Matches 407; Conservative 35; Mismatches 57;

Qy 1 AIGPVASLVVANAPVSPDGLRDAIVNVGVVPSPLITGKGRFQNLNVDPLTNHSLMS 60
Db 22 AIGPTADLTISNAEVSPPGFARQAVVNVVTPGPLVAGNKGDRFQNLNVDPLTNHSLMS 81
Qy 61 TSIHWHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 82 TSIHWHGFFQAGTNWADGPAFVNOCPISGHSFLYDFQVPDQAGTFWYHSHLSQYCDGL 141
Qy 121 RGPVVVYDPKDPHASYRDVDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSAST 180
Db 142 RGPVVVYDPKDPHASYRDVDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSAST 201
Qy 181 PTAALAVINVQHKRYRFLVSIQDNPNTFSDGNHNLTVIEVDGINSOPLVDSIQIFA 240
Db 202 TADLAVINVQHKRYRFLVSIQDNPNTFSDGNHNLTVIEVDGINSOPLVDSIQIFA 261
Qy 241 AQRYSFVLNANOTVGNVWRANPNFTGTFAGGINSAILRYOGAPVAPETTTQTTSVIPL 300
Db 262 AQRYSFVLNANOTVGNVWRANPNFTGTFAGGINSAILRYOGAPVAPETTTQTTSVIPL 321
Qy 301 IETNLHPLARMVPVPGSPGVDKALNLAFFNGTFFINNTATFPTVPVLLQILSGAQ 360
Db 322 NEVDLHPLATMAVPGSVAGVDTAIINMAFNGTNEFFINGASFVPTVPVLLQIISGAQ 381
Qy 361 TAQDLLPAGSVYPLPAHSTIETITLPATALAPGAPHPHLLHGHAFVAVRSAGSTTYNDP 420
Db 382 NAQDLLPSGSVYSLPSNADIEISFPATAAAGAPHPHLLHGHAFVAVRSAGSTTYNDP 441
Qy 421 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIVFAEDVADVKAANPV 480
Db 442 IFRDVVSTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIVFAEDVADVKAANPV 501
Qy 481 PKAWSDLCPYDGLSEANQ 499
Db 502 PKAWSDLCPYDGLDNDQ 520

RESULT 3

JC5357
laccase (EC 1.10.3.2) 5 precursor - white-rot fungus (Trametes villosa)
N:Alternate names: urushiol oxidase
C:Species: Trametes villosa (white-rot basidiomycete)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: JC5357
R:Yaver, D.S.; Golligly, E.J.
Gene 181, 95-102, 1996
A:Title: Cloning and characterization of three laccase genes from the white-rot basid
A:Reference number: JC5355; MUID:97128774; PMID:8973314
A:Accession: JC5357
A:Molecule type: DNA
A:Residues: 1-527 <YAV>
A:Cross-references: GB:I78078
C:Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phen
C:Genetics:
A:Gene: lcc5
A:Introns: 63/3; 86/3; 127/1; 165/1; 186/2; 220/2; 272/3; 357/3; 431/3; 470/3; 509/3
C:Superfamily: laccase
C:Keywords: oxidoreductase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-527/Product: laccase 5 #status predicted <MAT>

Query Match 71.8%; Score 1917.5; DB 2; Length 527;

Best Local Similarity 70.5%; Pred. No. 1.6e-133;
Matches 356; Conservative 47; Mismatches 93; Indels 9; Gaps 3;

Qy 1 AIGPVASLVVANAPVSPDGLRDAIVNVGVVPSPLITGKGRFQNLNVDPLTNHSLMS 60
Db 24 AIGPVTDLTISNADVTDPGITRAAVLAGGVFPGPLTGNKGRDEFQINVDNLNETLMS 83
Qy 61 TSIHWHGFFQAGTNWADGPAFVNOCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 84 TTIHWHGIFQAGTNWADGPAFVNOCPATGNSFLYDFHVPDQAGTFWYHSHLSQYCDGL 143
Qy 121 RGPVVVYDPKDPHASYRDVDNESTVITLTDWYHTAARLGRFPPLGADATLNLGLRSAST 180
Db 144 RGPLVYDPPDPNASLYDVDDTTVITLADWYHTAARLGRFPPLGADATLNLGLRSAST 203
Qy 181 PTAALAVINVQHKRYRFLVSIQDNPNTFSDGNHNLTVIEVDGINSOPLVDSIQI 238
Db 204 GGGATNLTVITVTOGKRYRFLVSIQDNPNTFSDGNHNLTVIEVDGINSOPLVDSIQI 263
Qy 239 FAQRYSFVLNANOTVGNVWRANPNFTGTFAGGINSAILRYOGAPVAPETTTQTTSVI 298
Db 264 FAGRYSFILNANOSIDNYWIRALPNVTGTTTGGVNSAILRYOAEDEIETTNATTSVI 323
Qy 299 PLIETNLHPLARMVPVPGSPGVDKALNLAFFNGTFFINNTATFPTVPVLLQILSG 358
Db 324 PLTETDLVPLDNPAAAGDPQGVGVDLAMSLDFSENGSNFFINNETFVPPTVPVLLQILSG 383
Qy 359 AQTADLLPAGSVYPLPAHSTIETITLPATAL----APGAPHPHLLHGHAFVAVRSAGST 413
Db 384 AQDAASLLPAGSVYPLPSNADIEISFPATAAAGAPHPHLLHGHAFVAVRSAGST 443
Qy 414 TYNNDPLFRDVGSTGTGTPAAGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIVFAEDVAD 473
Db 444 TFNANPVRRVTVSTGN--SGDNVTIRFQDNPFGWFLHCHIDPHLDAGFAIVGWDGAD 501
Qy 474 VKAANPVKAWSDLCPYDGLSEAN 498
Db 502 TASANPVTAWSDLCPYDGLDSSD 526

RESULT 4

S59533
laccase (EC 1.10.3.2) precursor - white-rot fungus (Trametes versicolor)
C:Species: Trametes versicolor (white-rot fungus)
C:Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 19-May-2000

pathogenesis.
C;Genetics:
A;Gene: lcc4
A;Introns: 62/3; 85/3; 126/1; 185/2; 217/2; 269/3; 335/3; 424/3; 463/3; 503/1
C;Superfamily: laccase
C;Keywords: oxidoreductase
F;1-22/Domains: signal sequence #status predicted <SIG>
F;23-520/Product: laccase 4 #status predicted <MAT>

Query Match 70.1%; Score 1871.5; DB 2; Length 520;
Best Local Similarity 68.5%; Pred. No. 3.8e-130;
Matches 342; Conservative 57; Mismatches 97; Indels 3; Gaps 2;

QY 1 AIGPVASLVNANPVPSPDGFELRDIAIVNGVVPSPPLITGKGGDRFQLNVDTFLNHSMKS 60
||| ||| :|| | ||| ||| :|| | ||| ||| :|| | ||| ||| :|| | |||
Db 23 AIGPVTGLTISNGDVSPDGTRAAVLANGVFPGLITGNKGDNFIQINIDLSNETMLKS 82
||| ||| :|| | ||| ||| :|| | ||| ||| :|| | ||| ||| :|| | |||
QY 61 TSIHHGFFOAGTNWADGPAFVNOCPTASGHSLFDHFVDPDAQGTFWYHSHLSFYQCDGL 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TSIHHGFFOKGTNWADGAFAFNOCPIATGNSFLYDFATDQAQTFWYHSHLSFYQCDGL 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 RGPVVVDPKDPHASRYDYDVNESVTIITLDMYHTAARLGPRFPLGDATLINGLRSAST 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 RGPVVVDPSDPHADLYDVDDETTIITLSDWYHTAASLGAAFPIGSDSTLINGLRFAAG 202
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 PTAALAVINVQHKKRYRFRLLVSICDDPNYFSIDGHNLTVEVDGINSQPILLVDSIOIFA 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 203 DSTDLAVITVEQGKRYRMRLLSCLSDPNYFSIDGHNMTIEADVANHPEPLTVDSIOIYA 262
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 AQRSFVLNANQTVGNVWRANPNFGVPGFAGGINSAILRYOGAPVAEPITTOTTTSVIPL 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 GORYSFVLTDODIDNYFIRALPSAGTISEDGGINSAILRYSGASEVDPPTTETTSVLPL 322
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 IETNLHLPARMPVPGSPTPGGVKALMAFNENGTNFINNATTPTPTVPVLQILSGAQ 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 DEANLVPLDSPAAPAGPNIGVDYALMDPFNDGTFINDVSFVSPVPVLQILSGTT 382
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 TAODLLPAGSVYPLPAHSHTTEITLPATAL-APGAPHFHLHGHAFAVVRSGASTTYNYND 419
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 SAADLLPGSILFVAPSNTSEIFPATNAPGNAPFHHLGHTFSIVRTAGSTDNTFVN 442
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 420 PIFRDVYSTGTPAAGDNWTIRFOTDNPMPFLHCCHIDFHLDAAGFAIVFAEDADVKAANP 479
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 PVRRDVTYTCT--VGDNVTIRTETDNPMPFLHCCHIDFHLDAAGFAIVFAEDADVKAANP 500
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 480 VPAWSDLCPITYDGLSEAN 498
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 501 PSTAWEDLCPTYNALDSSD 519
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
JC5355
laccase (EC 1.10.3.2) 3 precursor - white-rot fungus (*Trametes villosa*)
N;Alternate names: Urushiol oxidase
C;Species: *Trametes villosa* (white-rot basidiomycete)
C;Date: 28-May-1997 #sequence_revision 28-May-1997 #text_change 19-May-2000
C;Accession: JC5355
R;Xaver, D.S.; Golightly, E.J.
Gene 181, 95-102, 1996
A;Title: Cloning and characterization of three laccase genes from the white-rot basid
A;Reference number: JC5355; MUID:97128774; PMID:8973314
A;Accession: JC5355
A;Molecule type: DNA
A;Residues: 1-512 <YAV>
A;Cross-references: GB:I78076
C;Comment: This enzyme is a multi-copper enzyme which catalyzes the oxidation of phen
pathogenesis.
C;Genetics:
A;Gene: lcc3
A;Introns: 61/3; 84/3; 125/1; 163/1; 184/2; 211/2; 263/3; 330/3; 349/3; 416/3; 455/3;
C;Superfamily: laccase
C;Keywords: oxidoreductase
F;1-21/Domains: signal sequence #status predicted <SIG>

F;22-512/Product: laccase 3 #status predicted <MAT>

Query Match 66.4%; Score 1772; DB 2; Length 512;
Best Local Similarity 67.5%; Pred. No. 8e-123;
Matches 333; Conservative 38; Mismatches 112; Indels 10; Gaps 4;

Qy 1 AIGPVASIVLANAPVSPDGLRDAIVNGVSPSLITGKGRFQQLNVDTLTNHSMLKS 60
Db 22 SIGPVTELDIVNKVIADPGVARDIVLAGGTFPGPLITGKGDNRINNVKLVNQTMITS 81

Qy 61 TSIHHGFFQAGTNWADGAPFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 120
Db 82 TTIHHGFMQHTNWADGAPFVNOCPITASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGL 141

Qy 121 RGPVFWDPKPHASRYDVNDNESTVITLTDWYHTAARLGPREFLGADATLNGRST 180
Db 142 RGPLVIYDPHPDQAYLVDVDESVITLTDWYHTAARLGPREFLGADATLNGRST 196

Qy 181 PTAALAVINVOGKRYRFLRYSIDCPNFTSIDGHNLTIVEDGINSQPLLVDSIQIFA 240
Db 197 PTADLAVIEVQHKRYRFLRYSIDCPNFTSIDGHNLTIVEDGINSQPLLVDSIQIFA 256

Qy 241 AQRYSFVLNANQTVGNVWRANPN-FCIVGFAGGINSAILRYOGAPVAEPTTOTTIVIP 299
Db 257 AQRYSFVLNANQTVGNVWRANPN-FCIVGFAGGINSAILRYOGAPVAEPTTOTTIVIP 316

Qy 300 LIETNLHPLARMPVPGSPTPGGVDKALNLAFFNFTGTFANGINSAILRYOGAPVAEPTTOTTIVIP 359
Db 317 LWETDLHLTPDPRAGLPFGGVDHALNLTFFNGSEFFINDAPVPTVPVLLQILNGT 376

Qy 360 QTAODLLPAGSYVPLPAHSTIEITLPTALAPAGPHPHLGHAFVAVRSAGSTTYNND 419
Db 377 LDANDLLPGSYVPLPAHSTIEITLPTALAPAGPHPHLGHAFVAVRSAGSTTYNND 434

Qy 420 PIFRDVSTGTPAGDNTVIRFQDNPWFHCHIDHLDAGFAIYFAEDVADVKAANP 479
Db 435 PVKRTVTSIG--LAGDNTVIRFQDNPWFHCHIDHLDAGFAIYFAEDVADVKAANP 492

Qy 480 VPKAWSDLCPYD 492
Db 493 VPEDNKLCPYD 505

RESULT 7
S49120
laccase (EC 1.10.3.2) precursor - oyster mushroom
N:Alternate names: diphenol oxidase
C:Species: Pleurotus ostreatus (Oyster mushroom)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 11-Jun-1999
C:Accession: S49120
R:Giardina, P.; Cannio, R.; Martirani, L.; Marzullo, L.; Palmieri, G.; Sannia, G.
submitted to the EMBL Data Library, June 1994
A:Description: Gene structure of a phenol oxidase from the lignin degrading basidiomycet
A:Reference number: S49120
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-529 <GIA>
A:Cross-references: EMBL:Z34847; NID:G509380; PIDN:CAA84356.1; PID:G509381
C:Superfamily: laccase
C:Keywords: oxidoreductase

Query Match 65.3%; Score 1743.5; DB 2; Length 529;
Best Local Similarity 65.3%; Pred. No. 1.1e-120;
Matches 333; Conservative 53; Mismatches 105; Indels 19; Gaps 8;

Qy 1 AIGPVASIVLANAPVSPDGLRDAIV-----VNG---VWPSPLITGKGRFQQLNVDT 51
Db 24 AIGPTGDMYIVNEDVSPDGFTRSAVAVRSVPATDTPATATIPGVVQGNKGNFQQLNVNQ 83

Qy 52 LTNHSMKSTSIHHGFFQAGTNWADGAPFVNOCPITASGHSFLYDFHVPDQAGTFWYHSH 111
Db 84 %SDTTMLKTSIHHGFFQAGTNWADGAPFVNOCPITASGHSFLYDFHVPDQAGTFWYHSH 143

Qy 112 LSTQYCDGLRGPFWVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGPREFLGADATLI 171
Db 144 LSTQYCDGLRGPFWVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGPREFLGADATLI 202

Qy 172 NGIGRSASTPTAALAVINVOGKRYRFLRYSIDCPNFTSIDGHNLTIVEDGINSQPL 231
Db 203 NGRGFRAGGTSALAVINVESNKRYSRFLRYSIDCPNFTSIDGHSIQVLEDAVNIVPI 262

Qy 232 LVDSIQIFAQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTT 291
Db 263 VDSIQIFAQRYSFVLNANQTVGNVWRANPNFGTVGFAGGINSAILRYOGAPVAEPTT 322

Qy 292 TOTTSVPLIETNLHPLARMPVPGSPTPGGVDKALNLAFFNFTGTFANGINSAILRYOGAPVAEPTT 349
Db 323 TSSTST-PLEETNLVPLENPGAPVPGGADININLMAFDVTNFELTINGSPFKAPTA 381

Qy 350 PVLLQILSGAGTAQDILLPAGSYVPLPAHSTIEITLPTALAPAGPHPHLGHAFVAVRS 409
Db 382 PVLLQILSGAGTAQDILLPAGSYVPLPAHSTIEITLPTALAPAGPHPHLGHAFVAVRS 439

Qy 410 AGSTTYNNDPIFRDVTSTGTPAGDNTVIRFQDNPWFHCHIDHLDAGFAIYFAE 469
Db 440 AGSTTYNNDPIFRDVTSTGTPAGDNTVIRFQDNPWFHCHIDHLDAGFAIYFAE 498

Qy 470 DVADVKAANPVPKAWSDLCPYDGLSEANO 499
Db 499 DVTSTAP---PAAWDDLCPYDGLSEANO 525

RESULT 8
S62371
laccase (EC 1.10.3.2) precursor - oyster mushroom
C:Species: Pleurotus ostreatus (Oyster mushroom)
C:Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C:Accession: S62371; S62372; S49121; S54145
R:Giardina, P.; Aurilia, V.; Cannio, R.; Marzullo, L.; Amoresano, A.; Siciliano, R.;
Eur. J. Biochem. 235, 508-515, 1996
A:Title: The gene, protein and glycan structures of laccase from Pleurotus ostreatus.
A:Reference number: S62371; MUID:96184523; PMID:8654395
A:Accession: S62371
A:Molecule type: DNA
A:Residues: 1-533 <GIA>
A:Cross-references: EMBL:Z49075; NID:G785016; PIDN:CAA88895.1; PID:G785017
A:Accession: S62372
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-533 <GIZ>
A:Cross-references: EMBL:Z34848; NID:G785018; PIDN:CAA84357.1; PID:G785019
C:Genetics:

Query Match 65.3%; Score 1743.5; DB 2; Length 533;
Best Local Similarity 64.8%; Pred. No. 1.1e-120;
Matches 330; Conservative 49; Mismatches 109; Indels 21; Gaps 7;

Qy 1 AIGPVASIVLANAPVSPDGLRDAIVNGV-----VPSPLITGKGRFQQLNVV 49
Db 24 AIGPAGNMYIVNEDVSPDGFTRSAVAVRSVPATDTPATATIPGVVQGNKGNFQQLNVV 83

Qy 50 DTLTNHSMKSTSIHHGFFQAGTNWADGAPFVNOCPITASGHSFLYDFHVPDQAGTFWYH 109
Db 84 NOLSDTTMLKTSIHHGFFQAGTNWADGAPFVNOCPITASGHSFLYDFHVPDQAGTFWYH 143

Qy 110 SHLSTQYCDGLRGPFWVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGPREFLGADAT 169
Db 144 SHLSTQYCDGLRGPFWVYDPKDPHASRYDVNDNESTVITLTDWYHTAARLGPREFLGADAT 202

Db 438 IVKSLGGTP-NYVNPDRDVRVG-----GTGVVLRFKTDNPGPWFVHCHIDHWLEAGLAL 492
Qy 466 VFAEDVAD-----VKAAVVPKAWSDLCPIYDGL 494
Db 493 VFAEAPSIQROGVQSQVP-NNAWNOLCPKYAAL 524

RESULT 11

S68118
laccase (EC 1.10.3.2) 2 precursor [validated] - Rhizoctonia solani
C:Species: Rhizoctonia solani
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Apr-2000
R:Wahleithner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Golightly, E.J.; Halkier, T.; Kaur
Curr. Genet. 29, 395-403, 1996
A:Title: The identification and characterization of four laccases from the plant pathogen
A:Reference number: S68117; MUID:96171523; PMID:8598061

A:Accession: S68118
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-599 <WAH>
A:Cross-references: EMBL:Z54276
A:Experimental source: strain RS22
C:Genetics:
A:Gene: lcc2
A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 276/3; 408/3; 432/3; 469/2; 503/3; 555
C:Function:
A:Description: EC 1.10.3.2 [validated, MUID:96171523]
C:Superfamily: laccase
C:Keywords: copper; oxidoreductase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-599/Product: laccase 2 #status predicted <WAT>

Query Match 37.5%; Score 1000; DB 2; Length 599;

Best Local Similarity 38.7%; Pred. No. 7.5e-66;
Matches 226; Conservative 72; Mismatches 180; Indels 106; Gaps 14;

Qy 10 VANAPVSPDGLRDAIVNGVVPSPILITGKKGDRFQLNVDVTLTNHSLKSTSIHWHGFF 69

Db 28 VANGAVAPDGVTRNAVNVNGRFGPLITANKGDTLKITVRNKLSDPTMRRTIIHWHGLL 87

Qy 70 QAGTNWADGPAFVNPQCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPVYD 129

Db 88 QHRTAEDGPAFTQCPPIQPESYTYTGPLGDTGTWYHSHLSQYVDGLRGPVYD 147

Qy 130 KDPHASRYDVNDSVTITLTDWYHTAARLGRPRELGA-----DATLINGLGR---- 176

Db 148 HDPYRNYDVDDERTVFTLADWYHT-----PSEATIAITHDVLKTIIPDSGTINGKGYDPA 202

Qy 177 SASTPTAALA--VINVOHGKRYRFLRVISCDPNYTFSDGHNLTVIEVDGINSOPLIV 233

Db 203 SANTNNTTLENLYTLKVRGKRYRLINASAIASFRFGVQGHKCTIIEADGVLTKEPIDV 262

Qy 234 DSITQIFAAQRYSFVLNANTVGNVWRA-----NPN----- 264

Db 263 DAFDILAGORYSCILKADQDPSYWINAPITNVLTNVQALLVYEDDKRPTHYPWKPFLT 322

Qy 265 -----PGTVGFAGGINSAT-----LRYQGAP 285

Db 323 WKISNEIIYQWQHKGSHGKHGHHKVRVRAIGGVSGLSRSKRASDLSKAVELAAAL 382

Qy 286 VA-----EPTTQTTSVPIETNLHPLARMPVPGSPPTGGVDKALNLAFFNNGTNGFTN 340

Db 383 VAGEAELDKRONEDNSTIVLDETCLIPVQPGAGGSRPADVVPVPLDFCLNFANGLWTIN 442

Qy 341 NATFTPTTPVLLQILSGAQ--TAQDLLPAGSVYPLPAHSTIETILPATALAPGAPHPH 398

Db 443 NVSYSPDPPTLLKILTDKDKVDASDFTADEHTYILPKNOVVVELHKGQAL--GIVHPHL 500

Qy 399 LHGHAFVVRVRSAGSTTYNDPIFRDVGSTGTPAAGDNVTIRFQTDNPGPWFHCHIDPH 458

Db 501 LHGHAFDVVQ--FGDNAPNTVNPDRDV--GWTAG--VRIQRTDNPGPWFHCHIDWH 555

Qy 459 LDAGFAIVFAEDVADVKAANVPVK---AWSDLCPYDGLSEANQ 499
Db 556 LEEGFAMVFAEAPEDIKKSQSVKPDQGWKKLCEKYEKLPEALQ 599

RESULT 12

S68119

laccase (EC 1.10.3.2) 3 precursor - Rhizoctonia solani

C:Species: Rhizoctonia solani
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
R:Wahleithner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Golightly, E.J.; Halkier, T.; Kaur
Curr. Genet. 29, 395-403, 1996
A:Title: The identification and characterization of four laccases from the plant pathogen

A:Reference number: S68117; MUID:96171523; PMID:8598061

A:Accession: S68119

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-572 <WAH>

A:Cross-references: EMBL:Z54215; NID:g1150565; PIDN:CAA90942.1; PID:g1150566

A:Experimental source: strain RS22

C:Genetics:

A:Gene: lcc3

A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 380/3; 404/3; 441/2; 476/3;

C:Superfamily: laccase

C:Keywords: copper; oxidoreductase

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-572/Product: laccase 3 #status predicted <WAT>

Query Match 34.9%; Score 930.5; DB 2; Length 572;

Best Local Similarity 37.6%; Pred. No. 9.3e-61;

Matches 207; Conservative 68; Mismatches 206; Indels 69; Gaps 10;

Qy 7 SLVVANAPVSPDGLRDAIVNGVVPSPILITGKKGDRFQLNVDVTLTNHSLKSTSIHWH 66

Db 25 NLKISNGKIADPGVDERDATALVNGGYPGLITFANKGDTLKVKNKLTPMDPMTISIHWH 84

Qy 67 GFFQAGTNWADGPAFVNPQCPIASGHSFLYDFHVPDQAGTFWYHSHLSQYCDGLRGPV 126

Db 85 GLLQHRNADDDGPAFTQCPPIQPASYYTGPLGDTGTWYHSHLSQYVDGLRGLPLV 144

Qy 127 YDKDPHASRYDVNDSVTITLTDWYHTAAR-----LGRPFPLGADATLINGLGRSASTPT 182

Db 145 YDKDPHRRLLYDIDDEKTVLIIGDWYHTSSKAILATGNTITLQQPDSATINCKGRFPDPT 204

Qy 183 RA-----LAVINVOHGKRYRFLRVISCDPNYTFSDGHNLTVIEVDGINSOPLIV 238

Db 205 PANPNTLYTLKVRGKRYRLRVINSASIASFRMSIQGHKMTVIAADGVSTKPYQVDSFDI 264

Qy 239 FAAQRYSFVLNANTVGNVWRA----- 261

Db 265 LAGRIDAVVEANQEPDITYWINAPLTNVANKTAQALLIVEDDRRPPHPKGPYRKWSYSE 324

Qy 262 -----NPNFGTVGFAGGINSAT-----LRYQGPAPVAEPTTQTTSVPIETNLHPLA 309

Db 325 ALIKYKHKHGRGLSGHGLKARMMEGSLHLHGRDIVKRQNETTVV-MDETCLVPLE 383

Qy 310 RMPVPGSPTPGGVDKALNLAFFNNGTNGFTNINATPTPTVPVLLQILSGAQ--TAQDLLP 367

Db 384 HPGACAGCKPADLVLDLDFGVNFTTGHWMINGIPKHSMDPMTLLKILTDGVTESDFTQ 443

Qy 368 AGSVYPLPAHSTIETILPATALAPGAPHPHHLGHAFVVRVRSAGSTTYNDPIFRDVVS 427

Db 444 PEHTIILPKNKCVFENIKGNS--GLGIVHPHILHGHFTFDVVO-FGNPNPNYVNPDRDVVG 501

Qy 428 TCTPAAGDNVTIRFQTDNPGPWFHCHIDFHLDAAGFAIVFAEDVADVKA--ANVPKAW 484

Db 502 ----ATDEGVRPQFQTDNPGPWFHCHIDHWLEEGFAMVFAEAPKGGPKSPVPDQW 557

Qy 485 SDLCPIYDGL 494

Db 558 KDLCKRYGSL 567

RESULT 13

S68117

laccase (EC 1.10.3.2) 1 precursor - Rhizoctonia solani

C:Species: Rhizoctonia solani

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 13-Mar-1998

C:Accession: S68117

R:Wahleithner, J.A.; Xu, F.; Brown, K.M.; Brown, S.H.; Gollightly, E.J.; Halkier, T.; Kau

Curri. Genet. 25, 395-403, 1996

A:Title: The identification and characterization of four laccases from the plant pathogen

A:Reference number: S68117; MUID:96171523; PMID:8598061

A:Accession: S68117

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-576 <WAW>

A:Cross-references: EMBL:Z54275

A:Experimental source: strain RS22

C:Genetics:

A:Gene: lcc1

A:Introns: 45/1; 81/3; 102/3; 145/1; 146/1; 186/2; 273/3; 381/3; 405/3; 442/2; 477/3; 52

C:Superfamily: laccase

C:Keywords: copper; oxidoreductase

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-576/Product: laccase 1 #status predicted <MAT>

Query Match 33.8%; Score 901; DB 2; Length 576;

Best Local Similarity 37.7%; Pred. No. 1.4e-58;

Matches 212; Conservative 79; Mismatches 184; Indels 88; Gaps 18;

Qy 8 LVVANAPSPDGLRDAIVNGVWSPSLITGKGRFQNLNVVDLTNHSMLKSTSIHHHG 67

Db 26 LKISDGEIAPDGVKKNATLVNGYGPCLIFANKGTLKVKQNKLTNPENYRTTSIIHHG 85

Qy 68 FQAGTNADGPAFYNOCPISAGSHFLYDFHVPDQAGTFWHSLSLSTQYCDGLRPFVYV 127

Db 86 LQHRNADDGSPFTVQCPVPIRESYTYITLDDQTGYWHSLSQYVDGLRPLVIY 145

Qy 128 DKDPHASYVDNESTVITLTDWHTAAR-----LGRPPLGADATLNGLSRST 180

Db 146 DPKDPHRLYDVDDKTVLLIGDWHESKAILASGNITRQPSA---TINGKGRFDPD 202

Qy 181 PTAA----LAVINVQHKRYRFLVSIISCDPNYTESIDGHNLTVEVGINSOPLVDSI 236

Db 203 NTPANPDLYTLUKRGKRIYRUVINSSEIASFVSFGHKVTVIAADGVSTKPYQVDAF 262

Qy 237 QIFAAQRYSFVLNANQTVGNWVRAN----PNFGTVGF-----AGGI 274

Db 263 DILAGQRIDCVVEANQEPDTYINAPLTVNPKTAQALLVYEDRRPYHPKGPYKRVS 322

Qy 275 NSAILRYOG-----APVAEPT-----TTQTSVPIPLIETNLH 306

Db 323 SEAILIKYNNHKHKGRLSGHGLKARMIEGSHHLSRSVVKRQNETTVV-MDESKLV 381

Qy 307 PLARMPVPGSPTPG-GVDKALNLF--NFNGTNEFINNATPTPTVPVLLQTLSCAQ--T 361

Db 382 PL---EYFGACGSPADLVLDLTGLNFATGHWNINGIPYESKPIPTLLKLTDEDDGV 438

Qy 362 AODLLPAGSVYPLPAHSTIETLPATALAPGAPHPFLHGHAFAYVRSAGSTTYNYNDPI 421

Db 439 ESDFTKEETHVILPKNKICIEFNKNSGIP-ITHPVHLHGHTWDVVQ-FGNPNPNVNP 496

Qy 422 FRDVTSTGTPAAGDNVTIRFQTDNPGPWFLHCHIDFHLDAFGAIYFAEDVADVKAANVP 481

Db 497 RRDVV--GSTDAG--VRIQFTDNPGPWFLHCHIDHLEEGFAMVFAEPAEAVKGG---P 549

Qy 482 KA-----WSDLCPIYDGLSEAN 498

Db 550 KSAVVDSSQWEGLCGYDNWLKSN 572

RESULT 14

S72493

laccase (EC 1.10.3.2) precursor - Podospora anserina

N:Alternate names: benzenediol:oxygen oxidoreductase; urishiol oxidase

C:Species: Podospora anserina

C:Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000

C:Accession: S72493

R:Fernandez-Larrea, J.; Stahl, U.

Mol. Gen. Genet. 252, 539-551, 1996

A:Title: Isolation and characterization of a laccase gene from Podospora anserina.

A:Reference number: S72493; MUID:97071669; PMID:8914515

A:Accession: S72493

A:Molecule type: DNA

A:Residues: 1-621 <FER>

A:Cross-references: EMBL:Y08827; NID:g1729780; PIDN:CAA70061.1; PID:g1729781

A:Experimental source: strain ATCC 26003

C:Genetics:

A:Gene: lac2

A:Introns: 80/3; 111/1; 134/2

C:Function:

A:Description: catalyzes one-electron oxidation of mono-, di- and polyphenols, aminop

C:Superfamily: laccase

C:Keywords: copper; glycoprotein; oxidoreductase

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-48/Domain: amino-terminal propeptide #status predicted <PRO>

F:49-605/Product: laccase #status predicted <MAT>

F:74-209/Domain: amino-terminal beta-barrel #status predicted <BB1>

F:210-366/Domain: middle beta-barrel #status predicted <BB2>

F:431-528/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>

F:606-621/Domain: carboxyl-terminal propeptide #status predicted <CRP>

F:133,261,276,289,334,382,401,421,441/Binding site: carbohydrate (Asn) (covalent)

F:138,479/Binding site: copper (His) (type 2) #status predicted

F:140,183,185,481,548,550/Binding site: 2Cu-O cluster (His) (copper type 3) #status p

F:476,549,554/Binding site: copper (His, Cys, His) (type 1) #status predicted

Query Match 23.3%; Score 622.5; DB 2; Length 621;

Best Local Similarity 31.2%; Pred. No. 5.1e-38;

Matches 174; Conservative 71; Mismatches 184; Indels 129; Gaps 26;

Qy 15 VSPDGLRDAI-VWNGVVPSPILITGKGRFQNLNVVDLTNHSMLKSTSIHHHGFFQAGT 73

Db 92 LGPDGVKQKVLNVDIFGPTITANWGDWIOVNNLRTN---GTSIHHHGLRQKGT 147

Qy 74 NWADGPAFYVNOCP-ASGHSFLYDFHVPDQAGTFWHSLSLSTQYCDGLRPFVYVDPKDP 132

Db 148 NMHDGANGVTECPDPKGSRIYFRFA-QQYGTWYHSFSAQYGNVGVGTIV---NGP 203

Qy 133 HASRYDVDNESVTIPLTDWHTAARL-----GPRPLGADATLNGLSRSTPTAA 184

Db 204 ASVPYDID--LGVPFPTDYHKPADVLVEETMNGGP---PSDTVLFKGHGKNPQTGACK 258

Qy 185 LAVINVQHGKRYRFLVSIISCDPNYTESIDGHNLTVEVGINSOPLVDSIQIFAAQRY 244

Db 259 FANVLTPTGKRHLRIINTSTHDHFQKLQNHNTIIAADWVPVQAQTVDSLFLAVGORY 318

Qy 245 SFVLNANQTVGNWVRANPNCTVGFAGGI-----NSAILRYOGAPVAEPTTTOTT 295

Db 319 DVTIDANKSVGNWENAT-----FGGLACAGSLNHPHAPVFRYQAPNLTPLNIGT- 370

Qy 236 SVIPLIE-----TNLHPLARMPVPGS---PTPGVDVKALNLFNFGNTNFI----- 339

Db 371 ---PAADANCDNLNLTVPWSRSVPTSGTTPRP---NNTLPVSLTLGTPLFVWKNVSS 424

Qy 340 NNATPTPTVPVLLQILSGAQTAAQDLLPAGSVYPLPAHSTIET-----LPATALA 390

Db 425 INVMDKFTVDYVI-----AQN-----TSYP-POANVITVNSVNMWYTLIENDPTG 470

Qy 391 P-GAPHPFLHGHAFAYV---RSAG--STTYN------DPIRDRVYSTGTP 431

Db 471 PFSIPHPHMLHGHDFLVVGRSPDQAGVPQTRRNPATDMALLKSSNPVRDRDAM--LP 528

Qy 432 AAGDNVTIRFQTDNPGPWFLHCHIDFHLDAFGAIYFAEDVADV----- 475

Db 529 ANG-WLLIAFKSDNPGAWLFFHCHIAHWYSGGLSVQYLERPNDRNGFSQADKNHNNCN 587

Search completed: December 14, 2002, 08:29:03
Job time : 48 secs

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OM nucleic - nucleic search, using sw model
Run on: December 14, 2002, 05:08:11 ; Search time 3052 Seconds
(without alignments)
14303.476 Million cell updates/sec
Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gccatcgggccggtggcgag.....tgagcgaggctaaccagtga 1500
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
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- 23: em_pat.*
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- 30: em_htg_hum.*
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- 33: em_htg_mus.*
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- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1500	100.0	1500	6	AX384796	AX384796 Sequence
2	1500	100.0	1932	8	TVU44430	U44430 Trametes ve
3	1399.2	93.3	2408	8	AY049725	AY049725 Trametes
4	913.2	60.9	1563	8	AF414109	AF414109 Trametes
5	911.4	60.8	1563	8	TVE18012	Y18012 Trametes ve
6	899.6	60.0	1618	6	E02618	E02618 DNA encodin
7	899.6	60.0	1618	6	E02625	E02625 DNA sequenc
8	897	59.8	1497	6	E02226	E02226 CDNA encodi
9	894.8	59.7	1618	6	E02617	E02617 DNA encodin
10	894.8	59.7	1618	6	E02624	E02624 DNA encodin
11	892.2	59.5	1497	6	E02225	E02225 CDNA encodi
12	874.8	58.3	1572	6	AX002145	AX002145 Sequence
13	871.6	58.1	1572	6	AX002146	AX002146 Sequence
14	866.6	57.8	1829	8	AF176230	AF176230 Polyporus
15	861.4	57.4	1739	3	AB006824	AB006824 Trachyder
16	852.6	56.8	1557	8	AB072703	AB072703 Pycnoporu
17	843	56.2	1557	8	AF152170	AF152170 Pycnoporu
18	837.6	55.8	1869	8	AF491759	AF491759 Basidiomy
19	825	55.0	2127	8	TVU44851	U44851 Trametes ve
20	822.8	54.9	1845	8	AY081775	AY081775 Coriolus
21	771.8	51.5	2689	8	TMTLCCB	L49377 Trametes vl
22	771.8	51.5	2880	6	I65230	I65230 Sequence 3
23	755.4	50.4	7986	6	AX015224	AX015224 Sequence
24	729.8	48.7	2561	8	TVU44431	U44431 Trametes ve
25	722	48.1	2020	8	AF176231	AF176231 Polyporus
26	711.2	47.4	1915	8	AF491761	AF491761 Basidiomy
27	693.2	46.2	1694	8	AF176232	AF176232 Polyporus
28	639.2	42.6	1554	8	AF263467	AF263467 Coriolops
29	525.4	35.0	1602	8	AB020026	AB020026 Pleurotus
30	515.4	34.4	1822	6	E16453	E16453 Schizophyll
31	515.4	34.4	1822	6	AB015758	AB015758 Schizophy
32	513.6	34.2	1663	8	POPOX1R	Z34847 P.ostreatus
33	512.6	34.2	1713	8	POPOX2R	Z34848 P.ostreatus
34	509.4	34.0	1801	8	AB035409	AB035409 Lentinula
35	487	32.5	1772	8	POA75018	AJ005018 Pleurotus
36	472.6	31.5	1170	6	AR096341	AR096341 Sequence
37	472.6	31.5	1170	6	ARI40077	ARI40077 Sequence
38	472.6	31.5	1170	6	ARI56655	ARI56655 Sequence
39	462.8	30.9	2684	8	D13372	D13372 Coriolus ve
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41	454.8	30.3	2417	6	TMTLCCA	L49376 Trametes vl
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44	450.8	30.1	1397	8	AF297528	AF297528 Pleurotus
45	448.4	29.9	3963	8	AY081188	AY081188 Trametes

ALIGNMENTS

RESULT 1
AX384796
LOCUS AX384796 1500 bp
DEFINITION Sequence 1 from Patent WO0196543.
ACCESSION AX384796
VERSION AX384796.1 GI:19577931
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1
AUTHORS Hood,E., Howard,J.A., Bailey,M., van Gastel,F.J., Ward,M., Wang,H. and Woodard,S.
TITLE Method of increasing recovery of heterologous active enzymes produced in plants

JOURNAL Patent: WO 0196543-A 1 20-DEC-2001;
 Prodigene, Inc. (US); Genencor, Inc. (US)
 FEATURES Location/Qualifiers
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CDS
 275 a 551 c 402 g 272 t

BASE COUNT 275 a 551 c 402 g 272 t
 ORIGIN
 Query Match 100.0%; Score 1500; DB 6; Length 1500;
 Best Local Similarity 100.0%; Pred. No. 2.3e-216;
 Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCCATCGGGCGGTGGGAGCGCTGCTGCGGAGACGCCGCCGCTCGCCGCGAGCGGCTC 60
 DB 1 GCCATCGGGCGGTGGGAGCGCTGCTGCGGAGACGCCGCCGCTCGCCGCGAGCGGCTC 60
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QY	1081		ACCCGACAAAGACCTTCCTCGCAGGCTCTGTCTACCGCTCCCGGCCACTCCACCATC	1140
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QY	1141		GAGATCAGCTGCCCGGACCGCTTGGCCCGGGTGACCGACCCCTTCCACCTGCAC	1200
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QY	1201		GGTACGCGCTTGGCGGTGCTTCGAGCGGGGAGGACCACTATTAAGTACAGGACCGG	1260
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QY	1261		ATCTTCGCGACGCTGTGAGCAGCGGACCGCCGCGGGGAGCAACGTCACGATCCGC	1320
Db	1261		ATCTTCGCGACGCTGTGAGCAGCGGACCGCCGCGGGGAGCAACGTCACGATCCGC	1320
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QY	1381		GCGGCTTCGCGATCGTTCGAGAGGACGTTGGGACGTTGAGGCGGCGGACCCGGT	1440
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QY	1441		CCGAAGGCGTGGTGGGACCTGTGCCGATCTACGACGGGCTGAGCGAGGCTTAACAGTGA	1500
Db	1441		CCGAAGGCGTGGTGGGACCTGTGCCGATCTACGACGGGCTGAGCGAGGCTTAACAGTGA	1500

RESULT 2
 TVU44430
 LOCUS
 DEFINITION Trametes versicolor laccase I (lccI) mRNA, complete cds.
 ACCESSION U44430
 VERSION U44430.1 GI:1172162
 KEYWORDS
 SOURCE
 ORGANISM
 Trametes versicolor
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Aphyllophorales; Trametes.
 REFERENCE
 1 (bases 1 to 1932)
 Ong, E., Pollock, W.B. and Smith, M.
 Cloning and sequence analysis of two laccase complementary DNAs
 from the ligninolytic basidiomycete Trametes versicolor
 Gene 196 (1-2), 113-119 (1997)
 JOURNAL
 MEDLINE
 97464057

PUBMED 9322748
REFERENCE 2 (bases 1 to 1932)
AUTHORS Ong, E., Pollock, B. and Smith, M.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-1996) Edgar Ong, Biotechnology Lab, University of British Columbia, #237-6174 University Blvd, Vancouver, B.C. V6T 1Z3, Canada

FEATURES
Location/Qualifiers
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BASE COUNT 367 a 665 c 521 g 379 t
ORIGIN

Query Match 100.08; Score 1500; DB 8; Length 1932;
Best Local Similarity 100.08; Pred. No. 2.2e-216; Indels 0; Gaps 0;
Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCATCGGCGCGGTGGCGAGCTCGTTCGCGAAGCGCCCGCTCGCGCCGACGCGCTTC 60
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DB 304 CTTCCGGATCCATCGTGGTCAACGGCGTGGTCCCTTCCCGCTCATCACCAGGGAAG 363
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RESULT 3
AY049725
LOCUS
DEFINITION
ACCESSION
VERSION

2408 bp mRNA linear PLN 13-SEP-2001
Trametes versicolor laccase 1 (lacc1) mRNA, complete cds.
AY049725
AY049725.1 GI:15617226

KEYWORDS

SOURCE Trametes versicolor.
ORGANISM Trametes versicolor.
REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Trametes.
AUTHORS 1 (bases 1 to 2408)
TITLE Trametes versicolor laccase (lacI) mRNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2408)
AUTHORS McClean,K.H., O'Brien,M.M. and Dobson,A.D.W.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Microbiology, National Food Biotechnology Center, University College Cork, Cork, Ireland

FEATURES

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BASE COUNT 451 a 848 c 630 g 479 t
ORIGIN

Query Match 93.3%; Score 1399.2; DB 8; Length 2408;
Best Local Similarity 95.8%; Pred. No. 3.1e-201;
Matches 1437; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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Db 810 CTTCCGATGCCATCGTGGTCAACGGCGTGTCCCTTCCCGCTCATCAGGCGCAAGA 869
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Qy 1021 AAGCGACTTTCAGCGCGGACCGTCCCGGTACTCTCCAGATTCGAGCGGTGGCGAG 1080
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Db 1830 ACCGCAAGACCTGCTCCCTGCGAGGCTCGGTACCCGCTCCCGGCCACTCCACCATC 1889
Qy 1141 GAGATCAGCTGCGCGGACCGCTTGGCCCGGGGTGACCGCACCCCTTCCACCTGCAC 1200
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Db 1950 GGTACACCTTTCGCGGTCTTCGAGCGGGGAGCACACGATATACTACAAGACCGC 2009
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Qy 1381 GCGGCTTTCGCGATGCTTTCGAGAGAGAGTTCGGGACGCTGAAGGGGGGGAACCCGCTT 1440
Db 2130 GCGGCTTTCGCGATGCTTTCGCGAGAGAGTTCGGGATGTGAAGGGGGGAACCCGCTC 2189
Qy 1441 CCGAAGGCGGTGCGGACCTGTGCCCGGATCTACGACGGGTGAGCGAGGCTAACAGTGA 1500
Db 2190 CCGAAGGCGGTGCGGACCTGTGCCCGATCTACGACGGGTGAGCGAGGCGGACAGTGA 2249


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RESULT 4
AF414109
LOCUS AF414109 1563 bp mRNA linear PLN 26-SEP-2001
DEFINITION Trametes versicolor laccase B precursor (lac1) mRNA, complete cds.
ACCESSION AF414109
VERSION AF414109.1 GI:15778441
KEYWORDS
SOURCE
ORGANISM
Trametes versicolor.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Trametes.
REFERENCE
1 (bases 1 to 1563)
Jollivet,C., Madzak,C., Caminade,E. and Mouglin,C.
2,5-xylydine induced laccase from the basidiomycete Trametes
versicolor ATCC 32745
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1563)
Jollivet,C., Madzak,C., Caminade,E. and Mouglin,C.
Direct Submission
AUTHORS
Jollivet,C., Madzak,C., Caminade,E. and Mouglin,C.
JOURNAL
Submitted (23-AUG-2001) Unite de Phytopharmacie, INRA, Route de
Saint Cyr, Versailles 78026, France
FEATURES
Location/Qualifiers
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BASE COUNT 273 a 591 c 387 g 309 t 3 others
ORIGIN
Query Match 60.9%; Score 913.2; DB 8; Length 1563;
Best Local Similarity 75.6%; Pred. No. 4e-128;
Matches 1131; Conservative 0; Mismatches 366; Indels 0; Gaps 0;
QY 4 ATCGGCGCGGTGGCGAGCCTCGTGTGCGGAACGCCCGCGTCTCGCCCGACGGCTTCCTT 63
DB 67 ATCGGTCCGCTGGCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
QY 64 CGGGATGCCATCGTGTGCTAACGGCTGGTCCCTTCCCGCTCATCACCGGGGAAGGGA 123
DB 127 CGCAGCGCGTGTGCTGAACGGCGGCGACCCCTGGCGGCTTCTATCAGGGTAAACATGGG 186
QY 124 GACCGCTTCCAGCTCAACCTCGTTCGACACCTTGACCAACACAGCATGCTCAAGTCCACT 183
DB 187 GATCGCTTCCAGCTCAATGCTGACACCTTACCAACACACAGCATGCTGAAGACGACG 246
QY 184 AGTATCCACTGGACGGCTTCTTCAGGAGGAGGACCACTGGGAGAGACCGCGGCTTC 243
DB 247 AGTATTCACTGGCAGGTTTCTTCCAGAGGAGGACCACTGGGAGGAGGAGGAGGAGG 306
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Db 1387 CGCACGACACCCCGCGCGTGTCTCTCCACTGCCACATCGACTTCCACCTCGAGGCC 1446
Qy 1384 GCGTTCCGCGATCGTTCGCGAGAGAGTTCGCGACGTGAAGCGGGAACCCGCGTTCCG 1443
Db 1447 GCGTTCGCGTGTTCGCGAGGACATCCCGCGGTGCGGGAACCCGCGTCCC 1506
Qy 1444 AAGCGGTGCGGACCTGTGCGCGATACGACGCGGTGAGCGGAGGTACACAGTGA 1500
Db 1507 CAGCGGTGCGGACCTGTGCGCGACCTACGACGCGCGGACCCGAGGACAGTAA 1563

RESULT 5
TVE18012 TVE18012 Trametes versicolor mRNA 1563 bp mRNA linear PLN 02-FEB-1999
LOCUS Trametes versicolor mRNA for laccase.
DEFINITION Trametes versicolor mRNA for laccase.
ACCESSION Y18012
VERSION Y18012.1 GI:4218523
KEYWORDS laccase; lcc2 gene.
SOURCE Trametes versicolor.
ORGANISM Trametes versicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Trametes.
REFERENCE 1 (bases 1 to 1563)
AUTHORS Jonsson, L. and Nyman, P. O.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1563)
AUTHORS Jonsson, L. J.
DIRECT SUBMISSION
TITLE Submitted (27-AUG-1998) L. J. Jonsson, Lund University, Applied
JOURNAL Microbiology, P O Box 124, S-221 00, SWEDEN
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64. 1560
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BASE COUNT 270 a 600 c 387 g 306 t
ORIGIN

Query Match 60.8%; Score 911.4; DB 8; Length 1563;
Best Local Similarity 75.6%; Pred. No. 7.5e-128;
Matches 1131; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

Qy 4 ATCGGCGCGGTGCGAGCGTCTCGTCGGAACGCCCGCGTCTCGCGGACGCGTTCCTT 63
Db 67 ATCGGTCTGTGCGCGACCTCACCATCACCAGCGAGCGGTGAGCGGGTTTCT 126
Qy 64 CGGATGCCATCGTGTCAACGGCGTGTCTTCCCGCTCATCACCAGGGAAGGA 123

Db 127 CGCAGCGCGTGTGCGTGAACGGTGGCAACCCCTGGCCCTCTCATCACCGGTAAACATGGG 186
Qy 124 GACCGTTCAGCTCAACGTCGTGCGACACCTTGACCAACACACAGCATGCTCAAGTCCACT 183
Db 187 GATCGCTTCAGCTCAATGTATCGCAACCTCACGGACACACAGATGCTGAAGAGCACC 246
Qy 184 AGTATCCACTGGCAGCGCTTCTTCCAGCAGGAGCAACACTGGGAGAGACCGCGCTTC 243
Db 247 AGTATTCACGTGGCAGCGTTTCTTCCAGAGGGACCAACACTGGGCGGACGCTCCGCGCTC 306
Qy 244 GTCAACAGTGCCTATTTGCTTCGGGCATTCATTTCTGACAGCTTCCATGTCGCGGAC 303
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Db 487 GACGACACGGTTCATTACCTTGGCGATTGGTACACACCTGCCCGGAAGCTGGGCGCGCA 546
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Db 547 TTCCTCTCGGCGCGAGCCACTCTCATCAACGGTAAGGACGCTCCCGCAGCAGCACC 606
Qy 544 ACCCGCGCTGTGTGTATCAACGTCACGACCGGAAGCGCTACCGCTTCCGTTCTGTT 603
Db 607 ACCCGGACCTCACTGTATCAGCGTCATCCGGGTAAACGTTTACCCTTTCCGCTGTTG 666
Qy 604 TCGATCTCGTTCGCGACGAACTACAGTTGACGATCGACGGGCACTCTGACCGTCACTC 663
Db 667 TCCCTGTGTCGCGACCCCAACACCTTTCAGATCGATGCGGCAACATACGATCACTC 726
Qy 664 GAGGTGACGGTATCAACAGCAGCCTCTCTTGTGCACTCTATCCAGATCTTCCGCGCG 723
Db 727 GAGACCGACTCGATCAACACACGCGCGCTCTGTGTCGACTCCATTCAGATCTTCCGTCC 786
Qy 724 CAGCGCTACTCTTGTGTTGAATGCGAACCAGGTCGCGCACTACTTGGGTTCGCGCG 783
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Qy 784 AACCGAACTTCGGAACGGTTGGTTCGCGGGGGGATCAACTCGGCATCTCTCGGTAC 843
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Qy 844 CAAGCGCACAGTCGCGGAGCCCACTACGACCCAGAGAGCGTGGGTATCCCGCTTATC 903
Db 907 GATGGCGCGTGCATCGAGCCCAACACACGACGACCACTTCGACCGAGCGGCTCAAC 966
Qy 904 GAGAGAACTTGCACCCCTCGCTCGATGCTGTGCTGCGACGCGCGGACACCGCGGGC 963
Db 967 GAGGTCAACCTGCACCCGCTGTTGCCACCGCTTCCCTGGCTCTTCCGCTGCGGGTGGT 1026
Qy 964 GTCGACAAAGCGCTCAACCTTCGCGTTTAACTTCAACGCGCACCACTTCTTCATCAACAAC 1023
Db 1027 GTTGACCTGGCCATCATATATGCGGTTCACCTTCATGSCACCACTTCTTCATCAACGCG 1086
Qy 1024 GCGACTTTTCAGCGCGCGGACCGTCCCGGTACTCTCTCCAGATTCGTGAGCGGTGCGGAGAC 1083
Db 1087 GCGTCTTTTCAGCGCGCGGACCGTGCCTCTCTCTCCAGATCATCAGCGCGCGGAGAAC 1146
Qy 1084 GCACAAAGACTGTCTCTTCGAGGTCTGTCTACCGCTTCCCGGCGGCTCCACCATCCAG 1143
Db 1147 GCGAGGACCTCTCTCGCTCGGAGCGTATCTGCTCTCTCGCTCGGACCGCGGACATCGAG 1206
Qy 1144 ATCAGCGTTCGCGGACCGCTTGGCGCGGCTGCGCGGCTTCCCTTCCACTTCCAGCTGACCG 1203
Db 1207 ATCTCTTCCCGCGCACCGCTGCTGCCCGCGGTGCGCGCGGCTTCCACTTGCACGCG 1266

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QY 1204 CACGGCTTCCTCGGTCGTCAGCGGGGAGCACCAGGTATAACTACAAACGACCCGATC 1263
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QY 1384 GGCTTCGCGATCGTTTCGAGAGGAGCGTTCGCGACGTGAAGCGCGGAACCCGCTTCGG 1443
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Db 1447 GGCTTCGCGATCGTTTCGAGAGGAGCATCCCGGATGCGCATCGCGGAACCCCGCTTC 1506
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QY 1444 AAGCGGTGTCGACCTGTGCCCGATCTAGGAGCGGCTGAGCGAGGCTAACAGTGA 1500
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Db 1507 CAGGCGTGGTCCGACCTCTGCCGACCTAGGAGCGCGGACCCGAGCACCAGTAA 1563
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RESULT 6
LOCUS E02618
DEFINITION DNA encoding phenol oxidase(2).
ACCESSION E02618
VERSION E02618.1 GI:2170846
KEYWORDS JP 1990238885-A/2.
SOURCE Coriolus hirsutus.
ORGANISM Coriolus hirsutus
REFERENCE 1. (bases 1 to 1618)
AUTHORS Sugitara, J., Tsukamoto, A. and Kita, Y.
TITLE APHYLLOPHORALES; Coriolus.
HYPHOMYCOTA; Hymenomycetes; Homobasidiomycetes;
JOURNAL PHENOL OXIDASE GENE RECOMBINATION DNA, MICROORGANISM TRANSFORMED
WITH SAME RECOMBINANT DNA, CULTURE MIXTURE THEREOF AND PRODUCTION
OF PHENOL OXIDASE
PATENT: JP 1990238885-A 2 21-SEP-1990;
QJ1 PAPER CO LTD
COMMENT OS Coriolus hirsutus
PN JP 1990238885-A/2
PD 21-SEP-1990
PF 13-MAR-1989 JP 1989057952
PI SUGITARA JUN, TSUKAMOTO AKIRA, KITA YUKIO
PC C12N15/53,C12N1/21,C12N9/02,(C12N1:19),(C12N9/02, PC
C12N1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: strain=IFO 4917;
CC *source: clone=pVC p02;
FH Key Location/Qualifiers
FT 5'UTR 1..55
FT CDS 56..1618
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ORIGIN
Query Match 60.0%; Score 899.6; DB 6; Length 1618;
Best Local Similarity 75.0%; Pred. No. 4.4e-126;
Matches 1124; Conservative 0; Mismatches 374; Indels 0; Gaps 0;
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QY 181 ACTAGTATCCACTGGCAGCGCTTCTTCCAGGACGAGCAACAACTGGGCGACAGCCCGCG 240
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Db 299 ACAGATATCCACTGGCATGGCTTCTTCCAGAGGGGACAACTGGGTGATGTCCTCCGCG 358
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QY 241 TTCGTCAACAGTGGCCCTATTTGTCGGGCAATTCATTTCTGTACGACTTTCATATGTGCC 300
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Db 419 GACCAGGCGGTACTTCTGGTACACAGCCACTTGTCCACTCAGTACTGTGACGGCTG 478
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Db 479 CGGGTCTTTCGTGTACGATCCCAATGACCCGACGCGAGCTTGTATGACGTGAC 538
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QY 421 AAGCAGACGACGTCATCAGCTTGACCGACTGTATACACACCGCTGCCCGGCTCGGTCC 480
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Db 539 AATGACGACACCGCTGATCACCCCTCGCGGATTTGGTACACACTCCCGCAAGCTCGGCC 598
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QY 481 AGGTTCCCACTCGCGCGGACGCGACGCTCATCAATGGTCTTGGCGGCTCGGCTCCACT 540
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QY 541 CCACCGCGCGGCTTCTGTGTATCAACGTCACGACGGAAGCGCTACCGCTTTCGCTC 600
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Db 659 ACGCGCGGACCTCGCGGTCTCAACGTCACGAAGGCAAGCGCTACCGTTTCCGCTG 718
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QY 601 GTTTCGATCTCGTCGCGACCGCACTACAGTTCAGCATCGACGGGACAACTCTGACCGTC 660
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QY 661 ATGAGGTGCGAGGTATCAACAGCCAGCTCTCTTGTGTGACATCTATCAGATCTTCGCG 720
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Db 779 ATGAGGTGCGAGTCCATCACTCCCAACCTCTGCTGTTGATCCATCCAGATTTTCGCT 838
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QY 721 GCGACGCTACTCTCTTGTGTGATCGAACCAGGTCGGCAACTACTGGTCCGCG 780
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Db 839 GCGACGCTACTCTCTTGTGTGATCGAACCAGGTCGGCAACTACTGGTCCGCG 898
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QY 781 GCGAACCCTCAACTTCGGAACGGTTGGTTCGCGGGGGATCAACTCCGCGATCTTCGCG 840
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Db 899 GCGAACCCTCAACTTCGGAACGGTTGGTTCGCGGGGGATCAACTCCGCGATCTTCGCG 958
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QY 841 TACCAAGCGCACAGTTCGCGGACCCACTACGACCCAGACGAGCTGGTGTATCCGCTT 900
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Db 959 TACGACGCGCGCGACACCGGTTGAGCCACCCAGCTACGCTACGCGGACCAAGCCCTG 1018
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Db 1019 AAGGAGTTCGACTTGCACCCGCTTCGCCACCATGGCTGTGCCCGGTTTCCCGAGTCGCGGT 1078
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QY 961 GCGCTCGACAAGCGCTCAACCTCGCGTTTAACTTCAAGGGCAACCACTTCTTCATCAAC 1020
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Db 1079 GGTGTTGACAGCGCTATCAACATGGCTTCAACTTCAATGGTACCAACTTCTTCATCAAC 1138
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Db 1139 GCGCGAGCTTGTGCGCGCGCGCGCTGCGGTCTGCTCAGATCATCAGCGCGCGCGAG 1198
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Db 1319 GGTACAGCTTTCGGCGTGTTCGAGCGCGGGTGTTCGAGCGCGGCTTCAACTACGACACCC 1378
Qy 1261 ATCTTCCCGAGCTGTGAGCAGCGGACCGCCCGCGGGGCGGACAGCTCAGATCGC 1320
Db 1379 ATCTTCCCGAGCTGTGAGCAGCGGACCGCTCGGCGGGTGTGAGCAGCTCAGATCGC 1438
Qy 1321 TTCAGAGCGACAACCCCGCGCGTGTCTCTCCACTGCCACATCGACTTCCACTCGAC 1380
Db 1439 TTCGACCGACAACCCCGCGCGTGTCTCTCCACTGCCACATCGACTTCCACTTGGAG 1498
Qy 1381 GCGGCTTTCGGAGCTGTTCGCGAGGAGCGTTCGCGACGTGAAGCGGCGGAACCGGTT 1440
Db 1499 GCGGCTTTCGGTGTGTTCGAGGACATCCCGGAGCTCGCGTGGCGAACCCTGTC 1558
Qy 1441 CCGAAGCGGTGCGGACCTGTGCCGATCTACGACGGCTGAGGAGGCTTAACAGT 1498
Db 1559 CCTCAGCGGTGTCTGTGTGCCCCATCTATGACGCACCTCGATGTCAACGACAGT 1616

RESULT 7
E02625 LOCUS E02625 1618 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA sequence(OJ-POM2) coding for phenol oxidase.
ACCESSION E02625
VERSION E02625.1 GI:2170853
KEYWORDS JP 1990242685-A/2
SOURCE Coriolus hirsutus.
ORGANISM Coriolus hirsutus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Coriolus.
REFERENCE
AUTHORS Kojima,Y. and Kita,Y.
TITLE RECOMBINANT DNA OF PHENOL OXIDASE, YEAST TRANSFORMED WITH SAME
RECOMBINANT DNA, CULTURE MIXTURE THEREOF AND PRODUCTION OF PHENOL
OXIDASE
JOURNAL Patent: JP 1990242685-A 2 27-SEP-1990;
OJI PAPER CO LTD
COMMENT OS Coriolus hirsutus
PN JP 1990242685-A/2
PD 27-SEP-1990
PF 14-MAR-1989 JP 1989061859
PI KOJIMA YASUSHI, KITA YUKIO
PC C12N15/53,C12N1/19,C12N9/02,(C12N15/53,C12R1:645),(C12N1/19,
C12R1:865),
PC (C12N9/02,C12R1:865);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: strain-IFO 4917;
CC *source: library-Plasmid pVC P02;
FH Key Location/Qualifiers
FH 5'UTR 1..55
FH CDS 56..1618
FT /product='phenol oxidase'
FT /gene='OJ-POM2'.
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/db_xref='*taxon:5327'
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Best Local Similarity 75.0%; Pred. No. 4.4e-126;
Matches 1124; Conservative 0; Mismatches 374; Indels 0; Gaps 0;

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RESULT 8
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 ACCESSION
 E02226.1 GI:2170464
 VERSION
 JP 1990027986-A/2
 KEYWORDS
 Coriolus hirsutus.
 SOURCE
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 ORGANISM
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 Aphyllophorales; Coriolus.
 REFERENCE
 Kojima,Y., Shinohara,Y., Hirayanagi,M., Tsukamoto,A., Sugliura,J.,
 Sakano,M., Kita,Y. and Koide,K.
 PHENOL OXIDASE GENE (II)
 TITLE
 Patent: JP 1990027986-A 2 30-JAN-1990;
 JOURNAL
 OJI PAPER CO LTD
 COMMENT
 OS Coriolus hirsutus
 PN JP 1990027986-A/2
 PD 30-JAN-1990
 PF 15-JUL-1988 JP 1988175236
 PI KOJIMA YASUSHI, SHINOHARA YUKIKO, HIRAYANAGI MIEKO, PI
 TSUKAMOTO AKIRA,
 SUGIURA JUN, SAKAINO MAKOTO, KITA YUKIO, KOIDE KAZUO PC
 C12N15/53/C12N9/02.(C12N15/53,C12R1:645);
 CC strandedness: Single;
 CC topology: linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: clone-OJ-POM 2;
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Best Local Similarity 74.9%; Pred. No. 1.le-125;
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RESULT 9
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LOCUS E02617 1618 bp RNA linear PAT 29-SEP-1997
DEFINITION DNA encoding phenol oxidase(II).
ACCESSION E02617
VERSION E02617.1 GI:2170845
KEYWORDS JP 199023885-A/1.
SOURCE Coriolus hirsutus.
ORGANISM Coriolus hirsutus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Coriolus.
Sugiura, J., Tsukamoto, A. and Kita, Y.
PHENOL OXIDASE GENE RECOMBINATION DNA, MICROORGANISM TRANSFORMED
WITH SAME RECOMBINANT DNA, CULTURE MIXTURE THEREOF AND PRODUCTION
OF PHENOL OXIDASE
Patent: JP 199023885-A 1 21-SEP-1990;
OJI PAPER CO LTD
OS Coriolus hirsutus
PN JP 199023885-A/1
PD 21-SEP-1990
PF 13-MAR-1989 JP 1989057952
PI SUGIURA JUN, TSUKAMOTO AKIRA, KITA YUKIO
PC C12N1/53, C12N1/21, C12N9/02, (C12N1/21, C12R1/19), (C12N9/02, PC
C12R1/19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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CC *source: clone-pVC P09;
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Best Local Similarity 74.8%; Pred. No. 2.3e-125;
Matches 1121; Conservative 0; Mismatches 377; Indels 0; Gaps 0;
QY 1 GCCATCGGGCGGTCGAGCCCTCGTCTGGGGAACGCCGCCCTCTGCCCCGACGGCTTC 60
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DEFINITION DNA sequence(OJ-POM5) coding for phenol oxidase.
ACCESSION E02624
VERSION E02624.1 GI:2170852
KEYWORDS JP 1990242685-A/1.
SOURCE Coriolus hirsutus.
ORGANISM Coriolus hirsutus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Coriolus.
1. (bases 1 to 1618)
Kojima,Y. and Kita,Y.
RECOMBINANT DNA OF PHENOL OXIDASE, YEAST TRANSFORMED WITH SAME
FEDERATION DNA, CULTURE MIXTURE THEREOF AND PRODUCTION OF PHENOL
OXIDASE
Patent: JP 1990242685-A 1 27-SEP-1990;
QJI PAPER CO LTD
GS Coriolus hirsutus
PN JP 1990242685-A/1
PD 27-SEP-1990
PF 14-MAR-1989 JP 1989061859
PI KOJIMA YASUSHI, KITA YUKIO
FC C12N15/53,C12N1/19,C12N9/02,(C12N15/53,C12R1:645),(C12N1/19,
PC C12R1:865),
FC (C12N9/02,C12R1:865);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: strain-IFO 4917;
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Key Location/Qualifiers
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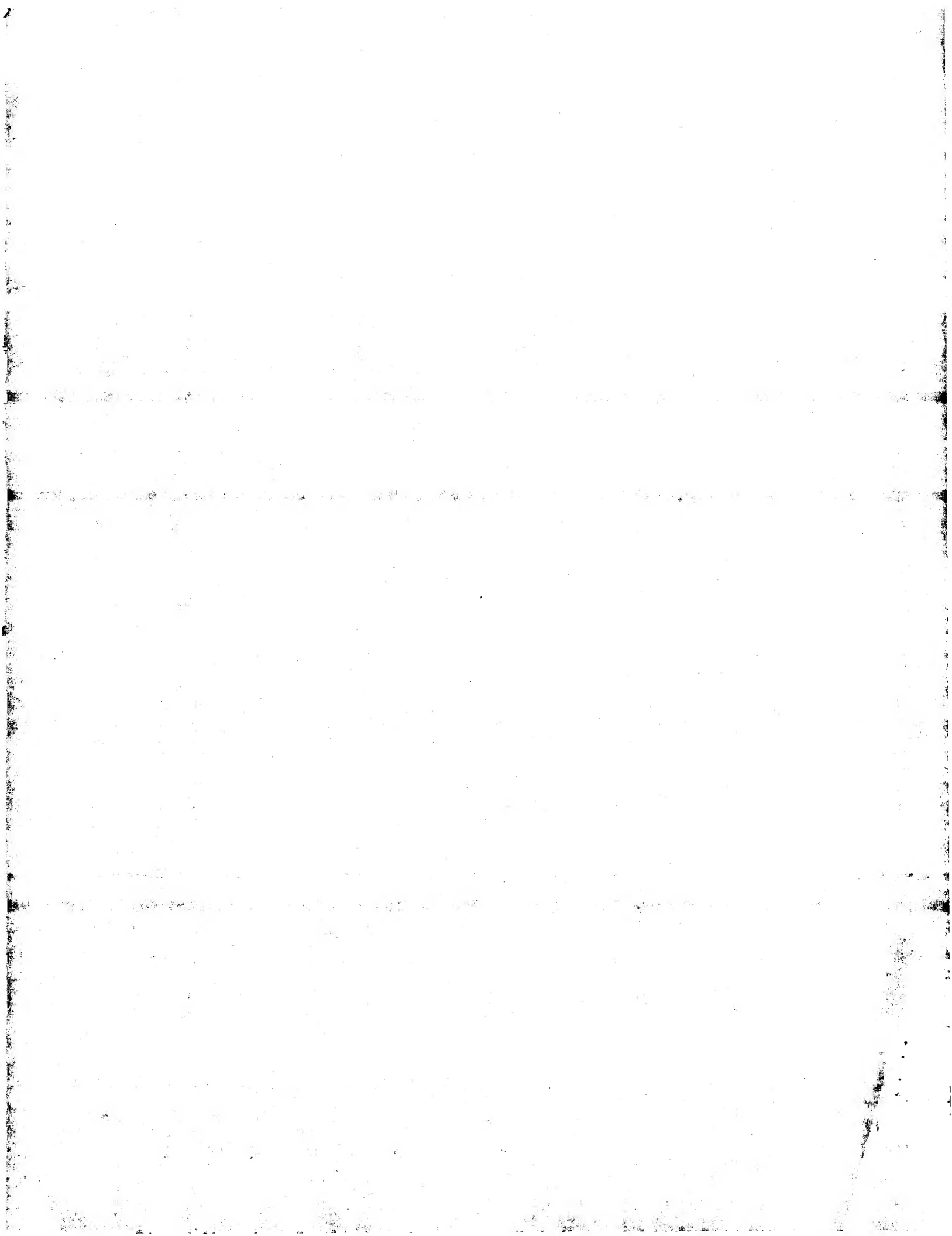
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Best Local Similarity 74.8%; Pred. No. 2.3e-125;
Matches 1121; Conservative 0; Mismatches 377; Indels 0; Gaps 0;
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Db	1219	CTCTCGTTCCCGCGGACTACTGTGCTCCGCGGTGCCCGCCACCCCTTCCACTTGCACGGT	1278
QY	1204	CACGCCCTCGGGTCGTTCCGACGGCGGGGAGCACACGCTATACTACAAGACCCCGATC	1263
Db	1279	CACACCTTCGCGCGTGTGCGCAGCGCGGAGCGCTGAGTACAACTACGACACCCCATC	1338
QY	1264	TTCCGCGACGCTCGTGACGCGGACCGCGCCCGCGGGCGACAACTCAGGATCCGCTTC	1323
Db	1339	TGGCGCAGCTCGTCAGCATGTTACCCCTGCACGGCGGATACGTCACCATTCGCTTC	1398
QY	1324	CAGACGACAAACCCCGGCGGTGTTCTCTCACTGCACATFCGACTTCCACTCGACGCG	1383
Db	1399	AGGACTGACAAACCTTGCCTGCTGTTCTCTCACTGCACATCGACTTCCACTTGGAGGCC	1458
QY	1384	GGCTTCGGATCGTTTCGCAGAGAGGCTTCCGACGCTGAAGCGCGGACCCCGTTCCG	1443
Db	1459	GGCTTCGCGGTGTCATGGCTTGAAGCATCCCGACACCAAGCGCGGACCCCTGTTCT	1518
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RESULT 13			
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LOCUS	AX002146	1572 bp	DNA linear PAT 10-MAR-2000
DEFINITION	Sequence 2 from Patent WO9855628.		
ACCESSION	AX002146		
VERSION	AX002146.1	GI:7241861	
KEYWORDS			
SOURCE	Trametes versicolor.		
ORGANISM	Trametes versicolor		
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;		
AUTHORS	Aphyllophorales; Trametes.		
TITLE	Pfaller,R. and Wich,G.		
JOURNAL	DNA SEQUENCES, EXPRESSION OF SAID DNA SEQUENCES, THERMOPILE LACASES CODED BY SAID DNA SEQUENCES AND THE USE THEREOF		
FEATURES	PATENT: WO 9855628-A 2 10-DEC-1998;		
source	PFALLER RUPERT (DE); WICH GUENTER (DE)		
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ORIGIN	Location/Qualifiers		
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Best Local Similarity	74.0%;	Pred. No. 7.3e-122;	
Matches 1105;	Conservative	0; Mismatches 389;	Indels 0; Gaps 0;
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QY	64	CGGATGCCATCGTGGTCAACGGCGTGGTCTCTCCCGCTCATCCCGGAAGAGGA	123
Db	139	CGCGGGCGGTCGTCGGAACGACGAGCGTCCCGGGCTCTCATACGGGCGCATGGGC	198
QY	124	GACGCTTCCAGCTCAAGCTCGTCGACACCTTGACCAACACGATGCTCAAGTCCACT	183
Db	199	GACGCTTCCAGATCAATGTGGTCAACAAGCTGTGCAACACACCATGCTTAATCGACC	258
QY	184	AGTATCCACTGGCAGCGCTTCTTCAGGACGAGGACCACTGGGACGACCGCGCTTC	243
Db	259	AGCATCCACTGGCAGCGCTTCTTCAGAAGGCGACGAATGGGCGGAGCGCTTCGCTC	318
QY	244	GTCACACAGTGGCTATGCTTCGGGATTCATTTCTGTAGCACTTCCATGTGCCGAC	303


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Db 1332 CACGCTCACGCTTCGCTGCTCGCCGAGCGGAGTAGCAGCTCTACAACTACGAC 1391
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Qy 1258 CCGATCTCCGCGAGCTGCTGAGACACGGGACACGCCCGCGGGGAGACAGCTACAGATC 1317
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Db 1392 CCCGCTCTACGCGAGCTCGTGAAGTACGGTACGC-----CTGGGACAACGTCACGATC 1445
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Qy 1318 CGCTTCACAGGAGACACCCCGGCGCTGCTTCTCCACTGCCACATCGACTTCCACCTC 1377
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Db 1446 CGCTTCACAGGAGACACCCCGGCGCTGCTTCTCCACTGCCACATCGACTTCCACCTC 1505
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Qy 1378 GACGCGGCTTCGCGATCGCTTCCAGAGGACGCTTCGGGACGCTGAAGGGGGAACCCG 1437
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Db 1506 GACGCGGCTTCGCGATCGCTTCCAGAGGACATCCCGAGCTGCTTCGCGGAACCCG 1565
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Qy 1438 GTTCCGAAGGCTGCTGCGGACCTGCTCCGATCTACGACGGCTGACGAGGCTTAACGAG 1497
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Db 1566 GTGCCCCAGGATGTTGACCTCTGCCCATCTATAACGGCTCGATCCCGAGTGACGAG 1625
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Qy 1498 TGA 1500
Db 1626 TAA 1628

RESULT 15
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LOCUS Trachyderma tsunodae mRNA for Bilirubin Oxidase, complete cds.
DEFINITION AB006824
ACCESSION AB006824
VERSION GI:3176127
KEYWORDS Bilirubin Oxidase.
SOURCE Trachyderma tsunodae (strain:K-2593) cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Trachyderma.
REFERENCE 1 (sites)
AUTHORS Iwamoto,H., Watanabe,H., Minakami,M., Hirose,J., Hiromi,K.,
Mukai,H., Yoshioka,H. and Kato,I.
TITLE Purification, Characterization, and Molecular Cloning of Bilirubin
Oxidase from Trachyderma tsunodae K-2593
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1739)
AUTHORS Iwamoto,H.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1997) Hiroyuki Iwamoto, Fukuyama University,
Faculty of Engineering, Gakuen-cho, Fukuyama, Hiroshima 729-02,
Japan (E-mail:iwamoto@fubac.fukuyama-u.ac.jp, Tel:0849-36-2111,
Fax:0849-36-2023)
FEATURES
Location/Qualifiers
source 1..1739
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strain="K-2593"
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Best Local Similarity 73.8%; Pred. No. 2.4e-120;
Matches 1109; Conservative 0; Mismatches 391; Indels 3; Gaps 1;
Qy 1 GCATCGGGCGGTCGGGACCCCTGCTCGCGAAGCCCGCTCTCGCCGAGCGCTTC 60
Db 76 GGGCTTGGCCCTCTGTGTCGACCTCACTGTCTCCAACGCCGTTATCTCCCGATGGCTTT 135
Qy 61 CTTCGGGATGCCATCGTGGTCAACGGGCTGCTCCCTTCCCGCTCATACACGGGAAGAAG 120
Db 136 GACCGTGATGCAATGTGCTCAACGGGTGCTTCCCTGCACCGCTCATCAGAGAAAGAAG 195
Qy 121 GGAGACCGCTTCAGCTCAACGCTGCTGACACCTTGACCAACACACAGCATGCTCAAGTCC 180
Db 196 GGGACCGCTTCCAGCTTAATGTGATCGACAACATGACGAACACACACCATGCTGAATCG 255
Qy 181 ACTAGTATCACTGGCACGGCTTCTCCAGGAGGACCAACTGGGCGAGACGGACCGCG 240
Db 256 ACGAGCATTCATGGCACGGCTTCTCCAGAGGAACTAATCTGGGCGGAGGTTGCT 315
Qy 241 TTGCTCAACAGTGCCTATTGCTTCGGGCAATTCATTTCTGTACGACTTCCATGTGCC 300
Db 316 TTTGTTAATAATGCCCATCGCCCGGCGCATTCGTTCTCTACGACTTCCGGGTCCCT 375
Qy 301 GACGAGCAGAGAGTCTGTGTACCAAGTATCTGTCTAGGCAATACTGTGAGGGGCTG 360
Db 376 GACCAAGCTGGCACCTTCTGTGTACCAAGCAATTTATCAACTAGTACTGCGATGGCTTA 435
Qy 361 CGAGACCGCTTCGCTGTAGTACGCCCAAGGATCCGACGCCGCCGCTACGATGTTGAC 420
Db 436 AGAGCTCTATGTGCTTACGACCCCAATGATCCACATGCGAATTTGTATGATGTCGAC 495
Qy 421 AACGAGACGAGTCTATCAGCTTGACGACTGTGTACCAACCGCTCGGCTCGGTC 480
Db 496 AACGATTCACCGCTCATAACCTTGCAGACTGTGTACCAAGTTGCGAGCGAGCTTGGGCCA 555
Qy 481 AGTTCCGACTCGGCGGAGCCCGCTCATCAATGGTCTTGGGCGGTGGGCTCCACT 540
Db 556 CGTTTCCGACTCGGCGGAGACTCAACAGTAAATCAACGGTCTTGGCGGCTCCCTCAGTACT 615
Qy 541 CCCACCGCGGCTTGTGTATCAACGCTCCAGCACGGAAGCGCTACCGCTCCGCTC 600
Db 616 CTAACGAGATCTGGCGGTGATATCGGTCAACCAAGGAACGTAACCGCTTCCGCTTG 675
Qy 601 GTTTCGATCTCGTGGACCCCGAATACAGCTTACAGCTGACGAGGCGACAACTGACCGTC 660
Db 676 ATATCCCTGTATCGACCCGCTTCCACACCTTCAGCATCGAGCGGTCTAGTACTATC 735
Qy 661 ATCAGGTCGACGGTATCAACAGCAGCGCTCTCTGTCGACTTATCAGATCTTCGCC 720
Db 736 ATTGAAGCTGACAGTGTGAACACCGAGCCTCTAGTTGTGACGACCATCCCATCTTTGCT 795
Qy 721 CGCAGCGCTACTCTTGTGTGTAATCGAACAACCGTGGCGCAACTACTGGTCCGC 780
Db 796 GCACAGCGCTACTCTTGTGTTTAGCGCGGTCAAGGACATCGAACAATACTGGATCCG 855
Qy 781 CGCAACCCGAACTTCGGAACGGTGTGGTTCGCGGGGGGATCAACTCGCGCATCTCGGC 840
Db 856 GCAGACCCCTAACTTCGGGCAACATGGATTTCGCCAGTGTGTATCAACTCTGCCATTTGCGC 915
Qy 841 TACCAAGCGGACAGTCCGCGACCCCACTAGGACCCAGACGAC--CTCGGTGATCCG 897
Db 916 TACGACGCTGTGCACCGCATGAGCCAACTGCGGTGCTTGTGCTCCGCTTCCGCTCAATCCT 975
Qy 898 CTTATCGAGGAACTTGACCCCCCTCGCTCGCATGCTGCTGTGCTCGCGTCCGCGCCACACC 957
Db 976 TTGCTCGAGACGAGGACTGCATCCGCTTGAAGACATGCCAGTCCGCGCGCCACCAAG 1035
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 05:09:06 : Search time 2135 Seconds
(without alignments)
11378.562 Million cell updates/sec

Title: US-09-786-960-1

Perfect score: 1500

Sequence: 1 gccatcgggccggtggcgag.....tgagcaggctaaccagtga 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: em_estin:*
4: em_estmu:*
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6: em_estpl:*
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8: em_htc:*
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10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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27: em_gss_fod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149.8	10.0	486	9	AT005119
2	138.8	9.3	419	9	AT004146
3	97	6.3	953	17	CNS0624A
4	90	6.0	501	9	AU082584
5	90	6.0	1020	17	CNS062GE
6	78.4	5.2	894	10	BE216612

7	72	4.8	612	14	B0826969
8	69.4	4.6	740	14	B0839421
9	69	4.6	509	13	BJ270853
10	69	4.6	511	13	BJ279320
11	68.4	4.6	509	14	B0760633
12	68.4	4.6	663	14	B0750959
13	68.2	4.5	519	10	AW671756
14	67.8	4.5	1003	17	CNS06601
15	67.6	4.5	662	13	B1959707
16	67	4.5	679	12	BG905538
17	66.6	4.4	790	10	BE040626
18	66.4	4.4	565	14	B0764122
19	66	4.4	429	12	BF201692
20	66	4.4	575	13	B1255523
21	66	4.4	641	13	B1959316
22	65.4	4.4	627	13	B1246521
23	64.6	4.3	539	14	B0578129
24	64.6	4.3	578	17	BH785519
25	64.6	4.3	627	17	AQ399182
26	64.4	4.3	440	10	B8423544
27	64.2	4.3	607	13	BH318801
28	63.2	4.2	617	13	B1289468
29	63.2	4.2	734	13	B1295794
30	62.8	4.2	453	12	BG606868
31	62.8	4.2	640	10	BE360607
32	62.6	4.2	843	17	CNS00CS1
33	62.2	4.1	461	14	B0578036
34	62.2	4.1	844	10	B8430514
35	62	4.1	655	13	BH370593
36	61.8	4.1	987	14	BQ752322
37	61.6	4.1	383	13	B1281253
38	61.6	4.1	631	13	B1277128
39	61.6	4.1	639	10	BE360567
40	61.2	4.1	332	13	B1286316
41	60.6	4.0	526	12	BG906020
42	60.6	4.0	559	13	BH418197
43	60.4	4.0	290	13	B1223789
44	60.2	4.0	932	17	CNS0072Q
45	60	4.0	476	6	BM441946

ALIGNMENTS

RESULT 1	AT005119	POMF01	Pleurotus ostreatus	cdna	linear	EST 25-MAR-2002
LOCUS	AT005119	486 bp	mrna			
DEFINITION	AT005119	sequence.				
ACCESSION	AT005119					
VERSION	AT005119.1	GI:13419977				
KEYWORDS	EST.					
SOURCE	Oyster mushroom.					
ORGANISM	Pleurotus ostreatus					
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;					
AUTHORS	Agaricales; Pleurotaceae; Pleurotus.					
TITLE	1 (bases 1 to 486)					
JOURNAL	Lee,S.H., Kim,B.G., Kim,K.J., Lee,J.S., Yun,D.W., Hahn,J.H., Kim					
MEDLINE	,G.H., Lee,K.H., Suh,D.S., Kwon,S.T., Lee,C.S. and Yoo,Y.B.					
COMMENT	Comparative Analysis of Sequences Expressed during the					
	Liquid-Cultured Mycelia and Fruit Body Stages of Pleurotus					
	ostreatus					
	Fungal Genet. Biol. 35 (2), 115-134 (2002)					
	21838565					
	Contact: Beom-Gi Kim					
	Division of applied microbiology					
	Institute of Agricultural Science and Technology(NIATST)					
	249 Seodundong Kweonseonku, Suwon 441707, Korea					
	Tel: 32-331-290-0347					
	Fax: 32-331-290-0399					
	Email: bgkimyes@da.go.kr					
	Submitted through BRIC(Biological Research Information Center) of					
	Korea					

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
11152876
2 (bases 1 to 953)
Malpertuy,A., Llorente,B., Blandin,G., Artiguenave,F., Wincker,P. and DuJon,B.
Genomic exploration of the hemiascomycetous yeasts: 10.
Kluyveromyces thermotolerans
FEBS Lett. 487 (1), 61-65 (2000)
20584720
11152885
3 (bases 1 to 953)
genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GBS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
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/evidence="not_experimental"
BASE COUNT 197 a 258 c 258 g 239 t 1 others
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Matches 343; Conservative 0; Mismatches 310; Indels 30; Gaps 3;

QY 73 ATCTGGTCAACGGGTGCTCCCTCCCGCTCATCACCGGGAAGGAGGACCGCTTC 132
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QY 133 CAGCTCAACGTCGTGACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATCCAC 192
DB 711 GAGGTGTAACCTGAAGAACGGTTCGAGGACCGCA-----ACAGTCGATGCAC 654

QY 193 TGGCAGCGTTTTCAGGCAGCGACCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 252
DB 663 TTCCATGGGCTGTTCCAGAACGGGACCACTCCATGGAGGGCCCTCCATGGTGGTGCAG 604

QY 253 TGCCCTATTGCTTCGGGCAATTCATTCGTACGACTTCCTCATGTCGCCGACGAGCA 312
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QY 313 AGTTCTGTGTACACATGATCTGTCTACGCAATCTGTGACGGGTGGAGGAGCGGTTTC 372
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QY 373 GTCTGTAGACCCCAAGGATCCGACGCGCCAGCGCTAGCATGTTGACAAACAGGACAG 432
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QY 433 GTCATCACGTTGACCGGACTGGTACCA---CACCGCTGCCCGGCTCGGTCCCGAGTTCCCA 489

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QY 490 CTCGGCGGCGACGCCAGCTCATCAATGCTTTGGCGGTGCGCCCTCCACTCCACCGCC 549
Db 378 AGTGTGTAACAATCTTACCACCGCGGGAACCTATTCGCCAGAACCTTATCATGAACAAC 319
QY 550 GGGCTTGTGTGATCAACGTCCAGCAGCGGAAAGCGGTACCGTTCCTGCTCGTTTCGATC 609
Db 318 AGGAACAATGACGTGGGAGGTCCAGCCGACACCACTGCTGCTGCTGATCAACACC 259
QY 610 TCGTGGGACCCGAACACTACAGCTTCAGCTTCAGGAGGCGCAACATCTGACCTCATFCAGAGT 669
Db 258 GGTGGCTTTGTGTCGCAGTACTTCTGGATCGAGGACCAAGATTCACGTTGTTGAGGTG 199
QY 670 GACGGTATCAACGACCGACCTCTCCTTGTTCGACTCTATCCAGATCTTCGCGCGGACGCG 729
Db 198 GACGGTATCTACCGAGAGAACACACCGCATGATCTATATCACTACGGCGCAGCGT 139
QY 730 TACTCCTTTGTGTTGAATCGAA 752
Db 138 TACACTTATTTGCTGCACACCAA 116

RESULT 4
LOCUS
AU082584
DEFINITION
AU082584 Rice shoot Oryza sativa (japonica cultivar-group) cDNA
clone S6123, mRNA sequence.
ACCESSION
AU082584
VERSION
AU082584.1 GI:6984608
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group).
ORGANISM
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 501)
Sasaki,T. and Yamamoto,K.
Rice cDNA from etiolated shoot (2000)
UNPUBLISHED (2000)
CONTACT: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel.: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT "RGP".

FEATURES
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Matches 153; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 523 GGGCGGTGGCTCCACTCCCGCGGCTTGCTGATCAACGTCCAGCAGGAAAG 582
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QY 583 CGCTACCGGTCGCTTCGTTTCGATCTCGTTCGCGACCCCGAACCTACAGTTCAGCATCGAC 642
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/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrMla6
) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give phagescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)

BASE COUNT 180 a 291 c 256 g 164 t 3 others

Query Match 5.2%; Score 78.4; DB 10; Length 894;
Best Local Similarity 54.8%; Pred. No. 1.1e-06;
Matches 204; Conservative 0; Mismatches 153; Indels 15; Gaps 2;
QY 25 GTCTGCGGACGCGCCGCTCTCGCCGAGCGCTTCCTCGGATGCCATCGTGGTCAAC 84
DB 214 GACATCTGTACCAAGTACAAAGTCCCGGACTGCTTCGAGAAGCTCCCGTACCGTCAAC 273
QY 85 GCGTGTGCTTCCCGCTCATACCGGGGAAGAGGAGACCGCTTCAGAGCTCAACGTC 144
DB 274 GCGAGCGCGCGCGCCGACCATCCGCGCCACGAGGCGA-----CACCATC 321
QY 145 GTCGACACCTTGACCAACACAGCATGCTCAAGTCCACTAGTATCCACTGGACGCGTTC 204
DB 322 GTCTCAACGTCACAAAGCTCGAGACCGGAGAACACCGCCATCCATCGGACGCGATC 381
QY 205 TTCCAGGAGGACCAACTGGGCGAGACGCGCTTCGTCACAGTCCCTATTGCT 264
DB 382 CGCCAGATTGACACGCGTGGCTGACGCGTGGCGGCTGACGAGTCCCGTCCCTATTGCT 441
QY 265 TCCGGCATTCATTCTGTACGACTTCCATGTGCCGACGAGGAGGAGTCTGGTAC 324
DB 442 CCGCGGAAACCTTCGCTTACAAATTC---GTCTGTCGACAGGCGCTGGCAGTAC 498
QY 325 CACAGTCACTCTACGCAATACTGTGACGGGCTGCGAGGAGCGTTCGTCGTGTACGAC 384
DB 499 CATGCGCACTAGGNNATGACGCGCTGGCGGNGCTCAACGGCATGATGCTGTGTCAGGTC 558
QY 385 CCAAGGATCCG 396
DB 559 CCGCGGCGATCG 570

RESULT 7
BQ826969
LOCUS BQ826969 612 bp mRNA linear EST 07-AUG-2002

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

gd49q07.x1 Moss EST library PPAS Physcomitrella patens cDNA clone
L-ASCORATE OXIDASE PRECURSOR 1, mRNA sequence.
BQ826969
BQ826969.1 GI:22132079
EST
Physcomitrella patens
Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella
1 (bases 1 to 612)
Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C., Clifton
, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood
, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T.,
Stepoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
, Waterston, R. and Wilson, R.
Leeds/Wash U Moss EST Project
Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Libraries were constructed by Dr. Stavros Bashardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 430.

FEATURES
Source

1. 612
/organism="Physcomitrella patens"
/db_xref="taxon:3218"
/clone="PEP_SOURCE_ID:PPAS021314"
/clone_lib="Moss EST library PPAS"
/dev_stage="protonemal, 7day old ABA-treated"
/lab_host="E.coli DH10b"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
EcoRI; 7-day-old protonemal tissue was incubated 10-4M ABA
for 16 hours before RNA isolation. cDNA was synthesised
from Amersham's cDNA Synthesis Plus kit and ligated with
EcoRI-NotI linkers for cloning in the EcoRI site of Lambda
ZapII (Stratagene). After packaging, the library was
propagated in E. coli XL-I Blue cells and amplified. The
library was excised by mass excision in SOLR cells and
ampicillin resistant transformants selected. Approximately
, 1,000,000 colonies were grown and recovered. The double
stranded plasmid library was recovered and used to
transform DH10b cells by electroporation. Clones
corresponding to abundant transcripts were identified by
colony hybridization using a cDNA probe derived from
untreated protonemal tissue, and eliminated from the
library, by rearraying."

BASE COUNT 128 a 198 c 152 g 134 t

Query Match 4.8%; Score 72; DB 14; Length 612;
Best Local Similarity 53.1%; Pred. No. 2.3e-05;
Matches 153; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 485 TCCCACTCGCGGAGCGGCGCTCATCAATGCTTGGGCGGTCCGCTCCACTCCCA 544
DB 236 TTCCACAGAATGCCACCTGCGCCCTGGCTGCTGCTGCAATCCAGCGACCTA 295
QY 545 CGCGCCGCTGTGTGATCAACGCTCCAGCAGGAAGCGCTACCGCTCCGCTCGTT 604
DB 296 GATCGCAGCTCATGTGTTGCCAGTCACCTCTGGAAGAGCTACCGCTGCGCATGCCCA 355

JOURNAL
COMMENT

Unpublished (2001)
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.

FEATURES

source

1. .509
Location/Qualifiers
/organism="Hordeum vulgare"
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/clone_lib="root, 3 week, waterlogged, cv Optic, EBR003"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old waterlogged barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SEERAD funded cereal IGF (Investigating
Gene Function) project."

BASE COUNT 98 a 181 c 140 g 90 t

ORIGIN

Query Match 4.6%; Score 68.4; DB 14; Length 509;
Best Local Similarity 56.6%; Pred. No. 0.00013;
Matches 154; Conservative 0; Mismatches 106; Indels 12; Gaps 1;
QY 25 GTCGTCGCGAACGCCCCGCTGTCGCCGCGAGCGGCTTCCTTCGGGATGCCATCGTGGTCAAC 84
Db 208 GACATCTCGTACCAAGTTAAAGTCCCGGACTGCTTCGAGAAGCTCGCGGTGACCGTCAAC 267
QY 85 GCGGTGTCTCTCCCGCTCATCACCGGAAGAGGAGACCGCTTCCAGCTCAAGTTC 144
Db 268 GCGGAGGCTCCCGCGCGACATCCACGCGACGCGGCGA-----CACCATC 315
QY 145 GTCGACACCTTGACACACACAGCATCTCAAGTCCACTAGTATCCACTGCGACGGGCTC 204
Db 316 GTCGTCGACGTCACACACAGCTCGACAGGAGACACCGCCATCCACTGGCAGGATC 375
QY 205 TTCAGGACGACCAACTGGGAGACGACCGCGGTCGTGTCACACAGTGCCTATTGCT 264
Db 376 CGCCAGATTGACAGCGCGTGGCGGCGGCTGCGCGGCTGACGAGTGCCTATCCTT 435
QY 265 TCCGGGATTCATTCTGTAGGACTTCATGT 296
Db 436 CCGGGGAAACCTTCACCTACAAATTCGTCT 467

RESULT 12

BQ750959/c

LOCUS BQ750959 663 bp mRNA linear EST 18-JUL-2002
DEFINITION EST631522 DSCT Colletotrichum trifolii cDNA clone pDSC1-67, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BQ750959.1 GI:21906364
Colletotrichum trifolii.
Colletotrichum trifolii
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 663)
Samad, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,
Cheung, F., and Fraser, C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
Other ESTs: EST631523
Contact: Deborah A. Samad
Department of Plant Pathology

University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSA677K More information is available at:
www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

FEATURES

source

1. .663
Location/Qualifiers
/organism="Colletotrichum trifolii"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSC1-67"
/clone_lib="DSCT"
/tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after
inoculation) grown in liquid culture (cutin minimal medium
containing 2% glucose)."
/lab_host="DH5alpha"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA. The cDNA was ligated into Lambda gtl1 from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
recombinants."

BASE COUNT 121 a 216 c 221 g 105 t

ORIGIN

Query Match 4.6%; Score 68.4; DB 14; Length 663;
Best Local Similarity 50.3%; Pred. No. 0.00014;
Matches 168; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
QY 1161 CGCCTTGGCCCGGGTCACGCGACCCCTTCCACCTGCACGGTCACGCTTCGCGGTCGT 1220
Db 645 CGCAAGCACCCGTTCCACCTGCACGCGCCACAGTTTCAGGTTCGCCACCGCTCGGCCGA 586
QY 1221 TCGCAGCGCGGGAGACACAGTATACACAGCCGATCTTCGCGAGACGTGTCGAG 1280
Db 585 GGACGCGCGGCTTCTCCGAGACCGGCTCGCCCTCCGCGGTACCCATGCGCCGCGA 526
QY 1281 CACGGGACGCCCGCGGGCGGACAGTCACGATCGCTTCCAGAGGACACCCCGG 1340
Db 525 CACCTCTGTCGAGGGGCAACGGCAACTTCGTATCCGCTTCGCGCGCCGACACCCCGG 466
QY 1341 GCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGACGCGGCTTCGCGATCGTGT 1400
Db 465 CGTGGCTGTTCCACTGCCACATCGAGTGGCAGATGACACAGGTTCTCGTCCGACCAT 406
QY 1401 CGCAGAGAGTTTCGCGACGTGAAGGCGGGAACCCGTTCCGAAGCGTGGTGGACCT 1460
Db 405 CGTCGAGGCGCCCGCGGCTGCGGGGCTGCTGGCGTCCCGAGGACCACTGGAGG 346
QY 1461 GTGCGGATCTACGACGCGGTGACGAGGCTAAC 1494
Db 345 GTGCGCGCGCGGGGTTCCCGACGAGGGCAAC 312

RESULT 13

AW671756

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AW671756 519 bp mRNA linear EST 19-JUL-2000
LOCUS IGL_351_B05_b1_A002 Light Grown 1 (LGI) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION AW671756
VERSION AW671756.1 GI:7535653
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor

Applicar

JOURNAL Patent: WO 0196543-A 1 20-DEC-2001;
Prodigene, Inc. (US); Genencor, Inc. (US)

FEATURES
source

1. 1500
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/db_xref="taxon:32644"
/note="Trametes sp."

CDS

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TVIEVDGINSOLFVDSQIFAAQRYSEVLNANOTVGNVWRANPFTGVGFAGINS
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TNFFINNAFTPTVPLVLIQSLGAOTADLLPAGSVYPLPAHSTIETLPTALAPG
APHPHGLHGAFAVRSAGSTVYNDPIFRDVSTGTPAAGDNWTRFQDNGPWF
LECHIDPHLDAGFAFYAEDVADVKAAHPVFAKMSDLCPIYDGLSEANQ"

BASE COUNT 275 a 551 c 402 g 272 t

Query Match 100.0%; Score 1500; DB 6; Length 1500;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCATCGGCGCGGTCGAGCCTCGTGTGCGGAACGCCCGCTCGCGCCGACGGCTTC	60
DB	1	GCATCGGCGCGGTCGAGCCTCGTGTGCGGAACGCCCGCTCGCGCCGACGGCTTC	60
QY	61	CTTCGGGATGCCATCGTGTCAACGGCGTGTCTCCCGCTCATCACGGGGAAG	120
DB	61	CTTCGGGATGCCATCGTGTCAACGGCGTGTCTCCCGCTCATCACGGGGAAG	120
QY	121	GGAGACCGCTTCCAGTCAACCTCGTGTGACACCTTGACCAACACAGCATGCTCAAGTCC	180
DB	121	GGAGACCGCTTCCAGTCAACCTCGTGTGACACCTTGACCAACACAGCATGCTCAAGTCC	180
QY	181	ACTAGTATCCACTGGCAGGCTTCTCAGGACGACGACCACTGGGACGAGGACCGCGG	240
DB	181	ACTAGTATCCACTGGCAGGCTTCTCAGGACGACGACCACTGGGACGAGGACCGCGG	240
QY	241	TTCTGCAACAGCTGCTTATTCCTCGGGCATTCATTTCTGACGATTCCTGTCGCC	300
DB	241	TTCTGCAACAGCTGCTTATTCCTCGGGCATTCATTTCTGACGATTCCTGTCGCC	300
QY	301	GACGAGGAGGAGCTTGTGTGACACAGTCACTGTCTACGCAATATCTGTGACGGGCTG	360
DB	301	GACGAGGAGGAGCTTGTGTGACACAGTCACTGTCTACGCAATATCTGTGACGGGCTG	360
QY	361	CGAGGAGGCTTGTGTGTGACGACCCAGGATCGCAGCGGCTACGATGTTGAC	420
DB	361	CGAGGAGGCTTGTGTGTGACGACCCAGGATCGCAGCGGCTACGATGTTGAC	420
QY	421	AACGAGGACGCTGCTATCAGCTGTGACGACGCTGACGACGCTGCGGCTCGGTC	480
DB	421	AACGAGGACGCTGCTATCAGCTGTGACGACGCTGACGACGCTGCGGCTCGGTC	480
QY	481	AGGTTCCACTCGGCGGACGCCAGCTCAATCAATGTGTTGGCGGTGCGGCTCCACT	540
DB	481	AGGTTCCACTCGGCGGACGCCAGCTCAATCAATGTGTTGGCGGTGCGGCTCCACT	540
QY	541	CCCACCGCGGCTGCTGTGATCAACGCTCAGGACGAGGAGCGGTACGCTTCGCTC	600
DB	541	CCCACCGCGGCTGCTGTGATCAACGCTCAGGACGAGGAGCGGTACGCTTCGCTC	600
QY	601	GTTCGATCTCGTGGACCCGAACTACAGCTTACAGCTGACGAGGACCAATCTGACGCTC	660
DB	601	GTTCGATCTCGTGGACCCGAACTACAGCTTACAGCTGACGAGGACCAATCTGACGCTC	660

DB	661	ATCGAGGTCGAGCGGTATCAACAGCAGCGCTCTCTCTGTCGACTCTATCCAGATCTTCGCC	720
QY	721	GGCAGCGCTACTCTCTGTTGTAATCGAACAACGCTCGGCAACTACTGGTCTCGC	780
DB	721	GGCAGCGCTACTCTCTGTTGTAATCGAACAACGCTCGGCAACTACTGGTCTCGC	780
QY	781	CGCAACCCGAACTTGGAAAGCTTGGGTTCCGCGGGGGATCAACTCGCGCATCTCGCC	840
DB	781	CGCAACCCGAACTTGGAAAGCTTGGGTTCCGCGGGGGATCAACTCGCGCATCTCGCC	840
QY	841	TACCAAGCGGACCACTGCGCGAGCCCACTAGGACCCAGACGCTCGGTGATCCCGTT	900
DB	841	TACCAAGCGGACCACTGCGCGAGCCCACTAGGACCCAGACGCTCGGTGATCCCGTT	900
QY	901	ATCGAGAGAACTTGACCCCTCGCTCGCATGCTGTGCTGGCAGCGCCGACGACCCCGG	960
DB	901	ATCGAGAGAACTTGACCCCTCGCTCGCATGCTGTGCTGGCAGCGCCGACGACCCCGG	960
QY	961	GGGTCGACAAAGGGGCTCAACTCGCGTTAACTTCAACGACCAACTTCTTCATCAAC	1020
DB	961	GGGTCGACAAAGGGGCTCAACTCGCGTTAACTTCAACGACCAACTTCTTCATCAAC	1020
QY	1021	AACGCGACTTTCAGCGCGCGGACCGCTCCCGTACTCTCTCCAGATCTGAGCGGTGCGCAG	1080
DB	1021	AACGCGACTTTCAGCGCGCGGACCGCTCCCGTACTCTCTCCAGATCTGAGCGGTGCGCAG	1080
QY	1081	ACCGCACAAAGCCTGCTCCCTGCGAGGCTCTCTACCGCGCTCCCGGCGGCACTTCCACCATC	1140
DB	1081	ACCGCACAAAGCCTGCTCCCTGCGAGGCTCTCTACCGCGCTCCCGGCGGCACTTCCACCATC	1140
QY	1141	GAGATCAGCTGCGCGGACCGCTTGGCCCGGGGTGACGCGGCGGCTTCCACGTCGAC	1200
DB	1141	GAGATCAGCTGCGCGGACCGCTTGGCCCGGGGTGACGCGGCGGCTTCCACGTCGAC	1200
QY	1201	GGTCAACGCTTTCGCGGCTGCTGCGAGCGCGGGGAGCACGCTATTAACGACGACCGG	1260
DB	1201	GGTCAACGCTTTCGCGGCTGCTGCGAGCGCGGGGAGCACGCTATTAACGACGACCGG	1260
QY	1261	ATCTTCGCGAGCTGCTGAGCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1320
DB	1261	ATCTTCGCGAGCTGCTGAGCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1320
QY	1321	TTCAGAGGAGCAACCGCGGCGGCTGCTCTCCACTGCGGCGGCGGCGGCGGCGGCGG	1380
DB	1321	TTCAGAGGAGCAACCGCGGCGGCTGCTCTCCACTGCGGCGGCGGCGGCGGCGGCGG	1380
QY	1381	CGGCGCTTCGCGGCTGCTGCGAGAGGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG	1440
DB	1381	CGGCGCTTCGCGGCTGCTGCGAGAGGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG	1440
QY	1441	CGAAGGCGGTGCGGAGCTTGGCGGCTGCGGAGCTGCGGAGGCTGAGCGGCTTAACGAGTGA	1500
DB	1441	CGAAGGCGGTGCGGAGCTTGGCGGCTGCGGAGCTGCGGAGGCTGAGCGGCTTAACGAGTGA	1500

RESULT 2

TVU44430

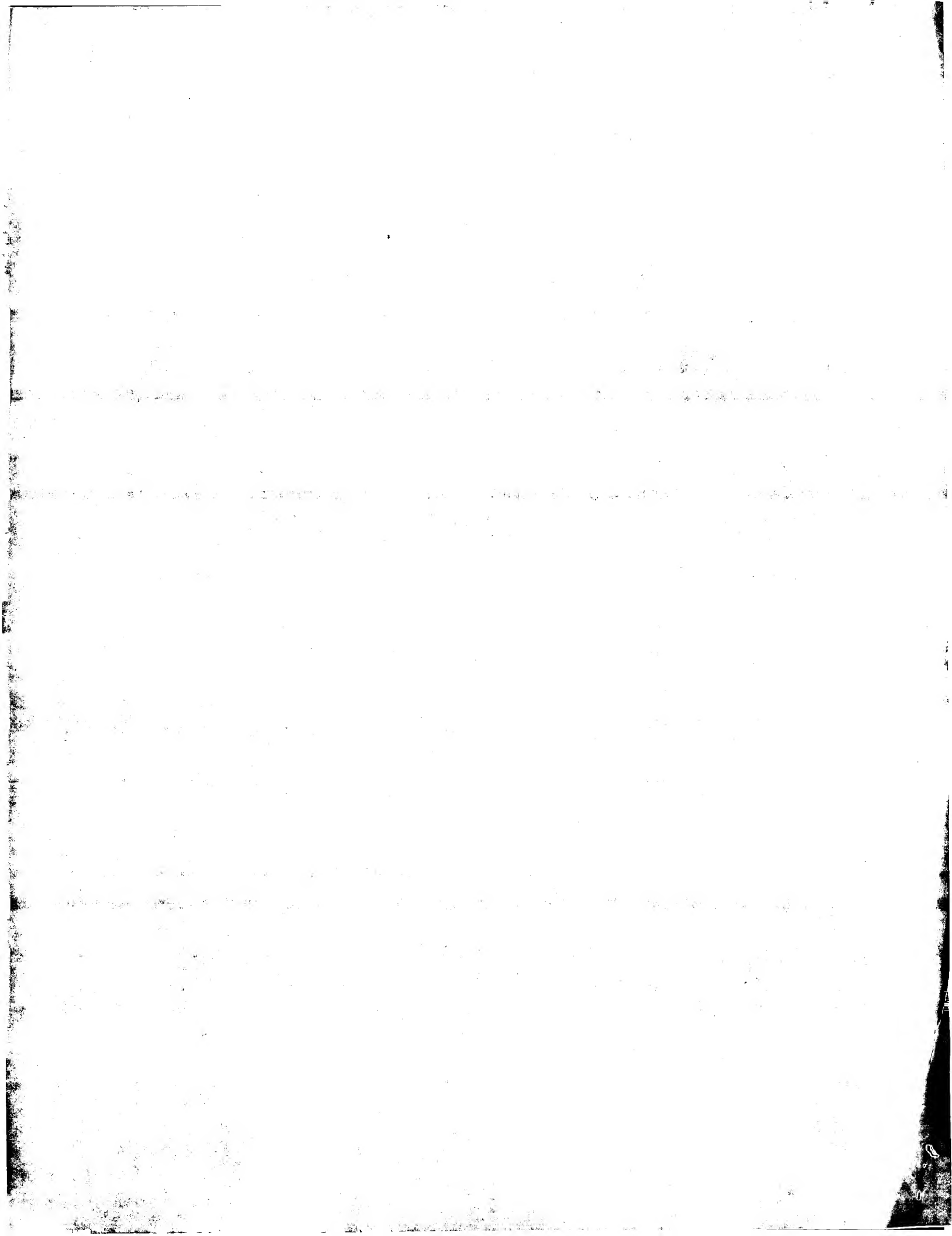
LOCUS
DEFINITION
Accession
VERSION
KEYWORDS
SOURCE
ORGANISM

TVU44430
Trametes versicolor laccase I (lcc1) mRNA
U44430
1932 bp linear
D44430.1
GI:1172162
PLN 17-APR-2001

Trametes versicolor.
Trametes versicolor
Aphyllophorales; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE

1 (bases 1 to 1932)
Ogawa, E., Pollock, W.B. and Smith, M.
Cloning and sequence analysis of two laccase complementary DNAs
from the ligninolytic basidiomycete Trametes versicolor
Gene 196 (1-2), 113-119 (1997)
97461057



9322748

PUBMED
 REFERENCE
 2 (bases 1 to 1932)
 AUTHORS
 Eng, E., Pollock, B. and Smith, M.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (02-JAN-1996) Edgar Ong, Biotechnology Lab, University of
 British Columbia, #237-6174 University Blvd, Vancouver, B.C. V6T
 123, Canada

FEATURES
 source

Location/Qualifiers
 1..1932
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 184..1743
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 IVNGVPSPLITCKKDRFQNLNVDTLTHSMUKSYSHWHGFFQAGTNWADGPAFV
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 RLVSICDPNTYSIDGNHNLTVIEVDGINSOPLLDVSIQIFAAORYSEVLNANQTVGN
 YWVRANPNFTVGFAGGINSAILRYOGAPVAEPVTTQTTSVIPLIETNHLPLAMPVP
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 PAGDNVITIRFDNPGMFWLHCHIDFHLDAFAIVEADVDVKAANPVPKAWSDLC
 FYDGLSEANO"

gene

CDS

BASE COUNT 367 a 665 c 521 g 379 t
 ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 1500; DB 8; Length 1932;
 Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GCCATCGGCGCGGTGGCGAGCTCGTCTCGGAAGCCCGCTCTCGCCGAGCGGCTC 60
 Db 244 GCCATCGGCGCGGTGGCGAGCTCGTCTCGGAAGCCCGCTCTCGCCGAGCGGCTC 303
 Oy 61 CTTGGGATGCCATCGTGGTCAAGCGGTGTCTCCCTTCCCGCTCATCACGGGAAG 120
 Db 304 CTTGGGATGCCATCGTGGTCAAGCGGTGTCTCCCTTCCCGCTCATCACGGGAAG 363
 Oy 121 GGAGACCGCTTCCAGCTCAAGCTCGTGACACCTTGACCAACACACGATGCTCAAGTCC 180
 Db 364 GGAGACCGCTTCCAGCTCAAGCTCGTGACACCTTGACCAACACACGATGCTCAAGTCC 423
 Oy 181 ACTAGTATCCACTGGCAGCGGCTTCTCCAGGACGACCAACTGGGAGACGACCGCGG 240
 Db 424 ACTAGTATCCACTGGCAGCGGCTTCTCCAGGACGACCAACTGGGAGACGACCGCGG 483
 Oy 241 TTCCTCAACAGTCCCTATGCTTCCGGGATTCATTTCTGTACGACTTCCATGTGCC 300
 Db 484 TTCCTCAACAGTCCCTATGCTTCCGGGATTCATTTCTGTACGACTTCCATGTGCC 543
 Oy 301 GACCAGGACGAGGCTTCTGTGTACACAGTCACTGTCTAGGCAATACTGTGACGGGCTG 360
 Db 544 GACCAGGACGAGGCTTCTGTGTACACAGTCACTGTCTAGGCAATACTGTGACGGGCTG 603
 Oy 361 CGAGGACGCTTGTGTGTACAGCCCAAGATCCGACCGCCAGCCGCTACGATGTTGAC 420
 Db 604 CGAGGACGCTTGTGTGTACAGCCCAAGATCCGACCGCCAGCCGCTACGATGTTGAC 663
 Oy 421 AACGAGACGAGCTCATCAGCTTGACCGACTGGTATACACACCGCTGCCGGCTGGTCCC 480
 Db 564 AACGAGACGAGCTCATCAGCTTGACCGACTGGTATACACACCGCTGCCGGCTGGTCCC 723
 Oy 481 AGGTTCCTCACTCGCGGCGGACGACGCTCATCAATGGCTTGGGGGTGGGCTCCACT 540

Db 724 AGTTTCCCACTCGGCGGAGCCAGGCTCATCAATGGTCTTGGGGGTGGGCTCCACT 783
 Oy 541 CCCACCGCGGCTTGTGTGTATCAACGCTCCAGCAGGAAACGCTACCGTTCGGTCTC 600
 Db 784 CCCACCGCGGCTTGTGTGTATCAACGCTCCAGCAGGAAACGCTACCGTTCGGTCTC 843
 Oy 601 GTTTCGATCTCGTGGAGCCGGAACCTACAGTTACAGTTCAGGTCGAGGGCACAATCTGACCGTC 660
 Db 844 GTTTCGATCTCGTGGAGCCGGAACCTACAGTTACAGTTCAGGTCGAGGGCACAATCTGACCGTC 903
 Oy 661 ATCGAGGTCGAGGCTATCAACAGCCAGGCTCTCTCTTGTGCTGACTCTATCCAGATCTTCGGC 720
 Db 904 ATCGAGGTCGAGGCTATCAACAGCCAGGCTCTCTCTTGTGCTGACTCTATCCAGATCTTCGGC 963
 Oy 721 GCGAGCGCTACTCTCTTGTGTGTAATCGAACAACGCTGGCAACTACTTGGTCCGC 780
 Db 964 GCGAGCGCTACTCTCTTGTGTGTAATCGAACAACGCTGGCAACTACTTGGTCCGC 1023
 Oy 781 GCGAACCAGAACTTCGGAACGTTGGGTTCCCGGGGGGATCAACTCCGCCATCTCGGC 840
 Db 1024 GCGAACCAGAACTTCGGAACGTTGGGTTCCCGGGGGGATCAACTCCGCCATCTCGGC 1083
 Oy 841 TACCAAGCGCACCACTCGCGAGCCCACTACGACCCAGAGAGACGCTCGGTGATCCCGTT 900
 Db 1084 TACCAAGCGCACCACTCGCGAGCCCACTACGACCCAGAGAGACGCTCGGTGATCCCGTT 1143
 Oy 901 ATCGAGAGAACTTGACCCCGCTCGCTCGCATGCTGTGCTGGCAGCCGACACCCGG 960
 Db 1144 ATCGAGAGAACTTGACCCCGCTCGCTCGCATGCTGTGCTGGCAGCCGACACCCGG 1203
 Oy 961 GCGCTGCACAAGGCGCTCAACCTCGCGTTAACTTCAACGACCACTTCTTCATCAAC 1020
 Db 1204 GCGCTGCACAAGGCGCTCAACCTCGCGTTAACTTCAACGACCACTTCTTCATCAAC 1263
 Oy 1021 AACCGGACTTTACGCGCGCGACCTCCCGGTACTCTCTCCAGATCTTGAAGGGTGGCGAG 1080
 Db 1264 AACCGGACTTTACGCGCGCGACCTCCCGGTACTCTCTCCAGATCTTGAAGGGTGGCGAG 1323
 Oy 1081 ACCGCAAGAAGCTTGCCTTGGAGGCTCTGTCTACCGGCTCCCGGCCACTTCCACCATC 1140
 Db 1324 ACCGCAAGAAGCTTGCCTTGGAGGCTCTGTCTACCGGCTCCCGGCCACTTCCACCATC 1383
 Oy 1141 GAGATACGCTTCCCGCGGACCGCTTGGCCCGGCTGACCGCGGACCGCTTCCACCTGCAC 1200
 Db 1384 GAGATACGCTTCCCGCGGACCGCTTGGCCCGGCTGACCGCGGACCGCTTCCACCTGCAC 1443
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 Db 1504 ATCTTCGCGAGCTCGTAGCAGCGGCGCGCGCGCGGGGAGCACAGTACAGTCCGC 1563
 Oy 1321 TTCAGACGACAAACCCCGGCGGCTGTCTCTCCACTGCCACATCGACTTCCACCTGCAC 1380
 Db 1564 TTCAGACGACAAACCCCGGCGGCTGTCTCTCCACTGCCACATCGACTTCCACCTGCAC 1623
 Oy 1381 GCGGGCTTCCGATCGTTCGAGAGAGAGCTTCCGGAGCTGGAAGGGGGGAAACCGGTT 1440
 Db 1624 GCGGGCTTCCGATCGTTCGAGAGAGAGCTTCCGGAGCTGGAAGGGGGGAAACCGGTT 1683
 Oy 1441 CCGAAGCGCTGCTGGACCTGTGCCGATCTACGACGGGCTGAGCGAGGCTTAACCACTGA 1500
 Db 1684 CCGAAGCGCTGCTGGACCTGTGCCGATCTACGACGGGCTGAGCGAGGCTTAACCACTGA 1743

RESULT 3

AY049725

LOCUS

DEFINITION

ACCESSION

VERSION

AY049725

Trametes versicolor laccase 1 (lccI) mRNA

AY049725

AY049725.1

2408 bp

linear

PLN 13-SEP-2001

complete cds.

GI:15617226

JOURNAL		Patent: WO 0196543-A 1 20-DEC-2001;	
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		APHPFLHGHAFVVRVSGSTTYNNDP IFRDVVSTGTPAAGDNVTIRFQTDNPGPW	
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ORIGIN			
Query Match	100.0%;	Score 1500;	DB 6; Length 1500;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1500;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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DB	1	GCATCGGCGCGTGGCGAGCTCTGTCGTCGGAGAGCCCGCTCGCGCCGACGGCTTC	60
QY	61	CTTCGGGATGCCATCTGCTGTCACAGCGGTGGTCCCTTCCCGCTCATCACCGGGAAGAAG	120
DB	61	CTTCGGGATGCCATCTGCTGTCACAGCGGTGGTCCCTTCCCGCTCATCACCGGGAAGAAG	120
QY	121	GGAGACCGGTTCCAGCTCAACGTCTGTCAGACCTTCACCAACACAGCATGCTCAAGTCC	180
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QY	241	TTCGTCAACCACTGCGCTATTTGCTCGGGCAATTCATTTCTGACGACTTCCATGTGCC	300
DB	241	TTCGTCAACCACTGCGCTATTTGCTCGGGCAATTCATTTCTGACGACTTCCATGTGCC	300
QY	301	GACGAGGAGCAAGCTTCTGGTACCAAGTATCTGCTACGCAATCTGTGACGGGCTG	360
DB	301	GACGAGGAGCAAGCTTCTGGTACCAAGTATCTGCTACGCAATCTGTGACGGGCTG	360
QY	361	CGAGGACCGTTCGTCGTGACGACCCCAAGGATCCGACGACCGGCTACGATGTTGAC	420
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DB	421	AACGAGACGAGTATCATGTTGACGATGTTGACGATGTTGACGATGTTGACGATGTTGAC	480
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DB	481	AGGTTCACCTCGCGCGGAGCGGACGCTCATCAATGCTTGGGCGGTGCGGCTCCACT	540
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QY	601	GTTTCGATCTCGTCGACCGGAACTACAGTTCAGTTCAGGAGGAGCAATCTGACCGCTC	660
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QY	901	ATCGAGACGAACCTTGCACCCCTCGCTCGCATGCTGTGCTGGCAGCCGACACCCCGGG	960
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QY	1441	CCGAAGGCGTGGTCGACCTGTCGCCGATCTACGACCGGCTGAGCGAGGCTTAACCACTGA	1500
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RESULT 2		1932 bp	mRNA	linear	PLN 17-APR-2001
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LOCUS	TV044430				
DEFINITION	Trametes versicolor laccase I (lccI) mRNA, complete cds.				
ACCESSION	U44430				
VERSION	U44430.1	GI:1172162			
KEYWORDS	Trametes versicolor.				
SOURCE	Trametes versicolor				
ORGANISM	Trametes versicolor				
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;				
AUTHORS	Aphylliphorales; Trametes.				
TITLE	1 (bases 1 to 1932)				
JOURNAL	Ong, E.L., Pollock, W.B. and Smith, M.				
MEDLINE	Cloning and sequence analysis of two laccase complementary DNAs from the ligninolytic basidiomycete Trametes versicolor				
	Gene 196 (1-2), 113-119 (1997)				
	97464057				

RESULT 2
TVU44430
LOCUS
DEFINITION
Trametes versicolor laccase 1 (lcc1) mRNA, complete cds.
ACCESSION
U44430
VERSION
U44430.1 GI:1172162
KEYWORDS
SOURCE
Trametes versicolor.
ORGANISM
Trametes versicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Trametes.
REFERENCE
1 (bases 1 to 1932)
AUTHORS
Ong E., Pollock W.B. and Smith M.
TITLE
Cloning and sequence analysis of two laccase complementary DNAs
from the ligninolytic basidiomycete Trametes versicolor
JOURNAL
Gene 195 (1-2), 113-119 (1997)
MEDLINE
97464057

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9322748

PUBMED

2 (bases 1 to 1932)

Onq, E., Pollock, B. and Smith, M.

Direct Submission

Submitted (02-JAN-1996) Edgar Onq, Biotechnology Lab, University of

British Columbia, #237-6174 University Blvd, Vancouver, B.C. V6T

123, Canada

Location/Qualifiers

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PIYGLSEANG"

BASE COUNT 367 a 665 c 521 g 379 t

ORIGIN

Query Match

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Matches 1500; Conservat 100.00; Pred. No. 0;

0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 GGAGACCGCTTCAGCTCAAGCTGTCGACACCTTGACACCAACAGCATGCTCAAGTCC 180

Db 364 GGAGACCGCTTCAGCTCAAGCTGTCGACACCTTGACACCAACAGCATGCTCAAGTCC 423

Qy 181 ACTAGTATCCACTGGCAGCGTCTTCCAGGACGACCACTGGGACAGGACCGCG 240

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Db 484 TTCGTCAACAGTGCCTTATGCTTCGGGCAATTCATTTCTGTACGACTTCCATGTGCC 543

Qy 301 GACGACGAGGAAGCTTCTGTACACAGTATCTGTCTACGCAATAGTGTGAGCGGTG 360

Db 544 GACGACGAGGAAGCTTCTGTGTACACAGTATCTGTCTACGCAATAGTGTGAGCGGTG 603

Qy 361 CGAGACCGTTCGTGTACGACCCCAAGGATCCGACGACCGCGCTACGATGTTGAC 420

Db 604 CGAGACCGTTCGTGTACGACCCCAAGGATCCGACGACCGCGCTACGATGTTGAC 663

Qy 421 AACGAGACGAGTTCATCAGTTGACCGACTGTGTACACACCGCTGCCCGCTCGGTCCC 480

Db 664 AACGAGACGAGTTCATCAGTTGACCGACTGTGTACACACCGCTGCCCGCTCGGTCCC 723

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Db 1684 CCGAAGCGGTGGTTCGACCTGTGCGCGATCTACACGGGCTGAGGAGGCTTAACAGTGA 1743

RESULT 3

AY049725

LOCUS

DEFINITION

AY049725

ACCESSION

VERSION

AY049725 2408 bp mRNA linear PLN 13-SEP-2001
Trametes versicolor laccase 1 (lacc1) mRNA, complete cds.
AY049725.1 GI:15617226

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2002, 06:12:08 ; Search time 3053 Seconds
(without alignments)
14298.791 Million cell updates/sec

Title: US-09-786-960-1
Perfect score: 1500
Sequence: 1 gcatcgccggtgag.....tgacgaggtaccagtga 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
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- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1500	100.0	1500	6	AX384796 Sequence
2	1500	100.0	1932	8	U4430 Trametes ve
3	483	32.2	2408	8	AY049725 Trametes
4	287	19.1	2127	8	U44851 Trametes ve
5	246	16.4	2689	8	L49377 Trametes vi
6	246	16.4	2880	6	I65230 Sequence 3
7	158	10.5	7986	6	AX015224 Sequence
8	59	3.9	2700	8	PGU65399 Basidiomyc
9	41	2.7	1829	8	AF176230 Polyporus
10	38	2.5	1563	8	AF414109 Trametes
11	38	2.5	1739	3	AB006824 Trachyder
12	38	2.5	1869	8	AF491759 Basidiomy
13	38	2.5	2020	8	AF176231 Polyporus
14	38	2.5	2043	8	AF388910 White-rot
15	38	2.5	2417	8	TMTLCCA
16	38	2.5	2418	6	I65229 Sequence 1
17	38	2.5	2780	8	BLACCASEG
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29	35	2.3	2812	8	TMTLCEE
30	35	2.3	2904	8	CRILIPHE
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33	35	2.3	3099	8	D84235 Coriolus ve
34	35	2.3	4996	8	AF414807 Trametes
35	33	2.2	1572	6	AX002145 Sequence
36	33	2.2	1572	6	AX002146 Sequence
37	33	2.2	3284	6	AX002152 Sequence
38	32	2.1	1584	8	AF185275 Ganoderma
39	32	2.1	2400	8	PGU65400 Basidiomyc
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41	30	2.0	2629	8	AF025481 Pycnoporu
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ALIGNMENTS

RESULT 1	AX384796	Sequence 1 from Patent WO0196543.	1500 bp	DNA	linear	PAT 19-MAR-2002
LOCUS	AX384796					
DEFINITION	AX384796					
ACCESSION	AX384796.1	GI:19577931				
VERSION	AX384796.1					
KEYWORDS						
SOURCE	unidentified.					
ORGANISM	unidentified.					
REFERENCE	1					
AUTHORS	Hood, E., Howard, J.A., Bailey, M., van Gastel, F.J., Ward, M., Wang, H. and Woodard, S.					
TITLE	Method of increasing recovery of heterologous active enzymes produced in plants					

JOURNAL Patent: WO 0196543-A 1 20-DEC-2001;
Prodigene, Inc. (US) ; Genencor, Inc. (US)
FEATURES Location/Qualifiers
source 1..1500
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/db_xref="taxon:32644"
/note="Trametes sp."
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1..1500
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RFLPDATYINGLRSASTPAALAVINVOHKRYRFLNISCDPNVTFIDGHNL
TIVIEGDIINQSLVDIQIFAAQRYSFVLNANQTVNFWNANFNGVTFAGGINS
AILRVGAPVAPETTOTTSVPLIETNLPLARMPVPGSPPTGGVDKALNFAFNG
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BASE COUNT 275 a 551 c 402 g 272 t
ORIGIN
Query Match 100.0%; Score 1500; DB 6; Length 1500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCATCGGGCGGTGGCGAGCTCGTGGGAAACGCCCGCTGTCGCCGCGAGCGGTTTC 60
Db 1 GCCATCGGGCGGTGGCGAGCTCGTGGGAAACGCCCGCTGTCGCCGCGAGCGGTTTC 60
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Qy 361 CGAGGACGTTCTGCTGTAGACCCCAAGATCCGACGCGCCAGCGCTACGATGTTGAC 420
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Qy 781 GCGAACCCGAACCTCGGAACGGTTGGTTGCGGGGGGATCAACTCCGCGATCTTCGCCG 840
Db 781 GCGAACCCGAACCTCGGAACGGTTGGTTGCGGGGGGATCAACTCCGCGATCTTCGCCG 840
Qy 841 TACCAAGCGCACCACTCGCGAGCCCACTAGACCCACAGCAGCTCGGTGTGATCCCGCTT 900
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Qy 901 ATCGAGACGAACCTGCAACCCCTCGCTCGATGCTGTGCTGGGAGCGCGACACCCGGG 960
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Qy 961 GGGGTGCAAGGCGCTCAACCTCGGTTTAACTTCAACGGGACCAACTTCTTCATCAAC 1020
Db 961 GGGGTGCAAGGCGCTCAACCTCGGTTTAACTTCAACGGGACCAACTTCTTCATCAAC 1020
Qy 1021 AACCGGACTTTCACGCGCGGACCGCTCCCGGTACTCTCCAGATTCGAGCGGTGGCGAG 1080
Db 1021 AACCGGACTTTCACGCGCGGACCGCTCCCGGTACTCTCCAGATTCGAGCGGTGGCGAG 1080
Qy 1081 ACCGCAACAGACCTGCTCCTCGAGCTGTCTACCGCTCCCGCCCACTCCACCATC 1140
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Qy 1141 GAGATCAGCTGCCCGCGACCGCTTTGGCCCGGGTGCACCGACCCCTTCCACCTGCAC 1200
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Qy 1201 GGTACGCTTCGCGGTGCTTCGAGCGGGGAGCACACGATATACATACACGACCGG 1260
Db 1201 GGTACGCTTCGCGGTGCTTCGAGCGGGGAGCACACGATATACATACACGACCGG 1260
Qy 1261 ATCTTCGCGACCTGCTGAGCAGGGGACCGCCCGCGGGGACCAACGTCACGATCCGC 1320
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Qy 1321 TTCAGACGACAAACCCCGGGCGGTGCTTCCACTGCGACATGCACTTCCACCTGCAC 1380
Db 1321 TTCAGACGACAAACCCCGGGCGGTGCTTCCACTGCGACATGCACTTCCACCTGCAC 1380
Qy 1381 GCGGCTTCGCGATCGTGTTCGAGAGGAGTTCGCGACGTTGAGGGCGGACCGGTT 1440
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Qy 1441 CCGAAGCGGTGGTGGACCTGTGCCGATCTAGACGGGTGAGCGAGGCTAACCACTGA 1500
Db 1441 CCGAAGCGGTGGTGGACCTGTGCCGATCTAGACGGGTGAGCGAGGCTAACCACTGA 1500
RESULT 2
TVU44430 1932 bp mRNA linear PLN 17-APR-2001
LOCUS
DEFINITION
Trametes versicolor laccase I (lccI) mRNA, complete cds.
ACCESSION
U44430
VERSION
U44430.1
GI:1172162
KEYWORDS
SOURCE
Trametes versicolor.
ORGANISM
Trametes versicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphylophorales; Trametes.
REFERENCE
1 (bases 1 to 1932)
Ong, E., Pollock, W.B. and Smith, M.
Cloning and sequence analysis of two laccase complementary DNAs
from the ligninolytic basidiomycete Trametes versicolor
Gene 196 (1-2), 113-119 (1997)
JOURNAL
MEDLINE
97464057

PUBMED 9322748
REFERENCE 2 (bases 1 to 1932)
AUTHORS Ong E., Pollock, B. and Smith, M.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-1996) Edgar Ong, Biotechnology Lab, University of British Columbia, #237-6174 University Blvd, Vancouver, B.C. V6T 1Z3, Canada

FEATURES
source Location/Qualifiers
1..1932
/organism="Trametes versicolor"
/strain="52J"
/db_xref="taxon:5325"
1..1932
/gene="lccI"
184..1743
/gene="lccI"
/EC_number="1.10.3.2"
/note="phenol oxidase"
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/translation="MGLRSEFFVTLALVARSALGIPVASILVLANPVSPDGLRDA
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PIYDGLSEANQ"

BASE COUNT 367 a 521 g 379 t
ORIGIN

Query Match 100.0%; Score 1500; DB 8; Length 1932;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCATCGGCGCGTGGCGAGCCTCGTCTCGGAACGCCCGCTCTCGCCCGAGCGCTC 60
DB 244 GCCATCGGCGCGTGGCGAGCCTCGTCTCGGAACGCCCGCTCTCGCCCGAGCGCTC 303
QY 61 CTTTCGGGATGCCATCGTGTGTCACAGCGGTGGTCCCTTCCCGGCTCATCACCGGGAAG 120
DB 304 CTTTCGGGATGCCATCGTGTGTCACAGCGGTGGTCCCTTCCCGGCTCATCACCGGGAAG 363
QY 121 GGAGACCGCTTCCAGCTCAACGCTGCTGACACCTTGACCAACACACAGCATGCTCAAGTCC 180
DB 364 GGAGACCGCTTCCAGCTCAACGCTGCTGACACCTTGACCAACACACAGCATGCTCAAGTCC 423
QY 181 ACTAGTATCCACTGGACAGCGCTTCTTCCAGGACAGGACCAACACTGGGACAGCGGCCGCG 240
DB 424 ACTAGTATCCACTGGACAGCGCTTCTTCCAGGACAGGACCAACACTGGGACAGCGGCCGCG 483
QY 241 TTCGTCAACAGTGCCTATTGCTTCGGGCAATTCATTTCTGACACATTCATGTCGTC 300
DB 484 TTCGTCAACAGTGCCTATTGCTTCGGGCAATTCATTTCTGACACATTCATGTCGTC 543
QY 301 GACGAGGAGGAACGTTCTGGTACACAGTCACTCTGCTACGCAATACTGTGACGGGCTG 360
DB 544 GACGAGGAGGAACGTTCTGGTACACAGTCACTCTGCTACGCAATACTGTGACGGGCTG 603
QY 361 CGAGGACCGTTCGTGTGACGACCCCAAGGATPCGACGCCAGCGCTACGATGTTGAC 420
DB 604 CGAGGACCGTTCGTGTGACGACCCCAAGGATPCGACGCCAGCGCTACGATGTTGAC 663
QY 421 AACGAGACACGCTCATACGTTGACCGACTGCTACACACACCGCTGCCCGGCTCGTCCC 480
DB 664 AACGAGACACGCTCATACGTTGACCGACTGCTACACACACCGCTGCCCGGCTCGTCCC 723
QY 481 AGGTTCCCACTCGGCGGACGACCGCTCATCAATGGTCTTGGGCGGTTCGGGCTCCACT 540
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RESULT 3
AY049725
LOCUS
DEFINITION
ACCESSION
VERSION

AY049725
Trametes versicolor laccase 1 (lacc1) mRNA, complete cds.
AY049725
AY049725.1 GI:15617226

2408 bp
mRNA
linear
PLN 13-SEP-2001

Db 724 AGGTTCCACTCGGCGGACGACCGCTCATCAATGGTCTTGGGCGGTCCGCTCCACT 783
QY 541 CCACACCCCGCGCTTGTGTGATCAAGCTCCAGACGGAAGCGCTACCGCTTCCGCTCTC 600
Db 784 CCACACCCCGCGCTTGTGTGATCAAGCTCCAGACGGAAGCGCTACCGCTTCCGCTCTC 843
QY 601 GTTTCGATCTCGTGGACCCGAACTACACGTTTCAGCATCGACGGGCAACAATCTGACCGTC 660
Db 844 GTTTCGATCTCGTGGACCCGAACTACACGTTTCAGCATCGACGGGCAACAATCTGACCGTC 903
QY 661 ATCGAGTTCGACGGTATCAACAGCCAGCTCTCTTGTGACATCTATCCAGATCTTCGCC 720
Db 904 ATCGAGTTCGACGGTATCAACAGCCAGCTCTCTTGTGACATCTATCCAGATCTTCGCC 963
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Db 1024 GCGAACCCGAACTTCGGAACGTTGGTTCGCGGGGGGATCAACTCCGCCATCTCTCGGC 1083
QY 841 TACCAAGCGCCACAGTCGCGGAGCCCACTACGACCCAGACGAGTGGGTGATGCCGCTT 900
Db 1084 TACCAAGCGCCACAGTCGCGGAGCCCACTACGACCCAGACGAGTGGGTGATGCCGCTT 1143
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Db 1144 ATCGAGACGAACTTGCACCCCTCGCTCGCATGCCTGTGCTGGCAGCCGACACCGGG 1203
QY 961 GCGCTCGACAAAGCGCTTCAACCTCGCTTTAACTTCAACGGCACCAACTTCTTCATCAAC 1020
Db 1204 GCGCTCGACAAAGCGCTTCAACCTCGCTTTAACTTCAACGGCACCAACTTCTTCATCAAC 1263
QY 1021 AACCGACTTTTACGCGCGGACCGCTCCCGTACTCTCTCAGATCTGAGCGGTGCGCAG 1080
Db 1264 AACCGACTTTTACGCGCGGACCGCTCCCGTACTCTCTCAGATCTGAGCGGTGCGCAG 1323
QY 1081 ACCGCAACAGCTGCTTCCCTGAGGCTCTGTACCCGCTCCGCGCCACTCCACCATC 1140
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Db 1684 CCGAAGCGGTGTCGACCTGTGCCCGATCTACGACGGGTGAGCGAGGCTAACACAGTGA 1743

KEYWORDS

Trametes versicolor.
Trametes versicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Trametes.

REFERENCE

1 (bases 1 to 2408)
McClean,K.H., O'Brien,M.M. and Dobson,A.D.W.
Trametes versicolor laccase (laci) mRNA sequence

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 2408)
McClean,K.H., O'Brien,M.M. and Dobson,A.D.W.

AUTHORS

Direct Submission

TITLE

Submitted (31-JUL-2001) Microbiology, National Food Biotechnology

JOURNAL

Center, University College Cork, Cork, Ireland

FEATURES

Location/Qualifiers

1..2408

/organism="Trametes versicolor"

/strain="CUI"

/db_xref="taxon:5325"

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/gene="laci"

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/note="phenol oxidase"

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/db_xref="GI:1561727"

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RLVSTCDPNYTFSDGHNLVIEVDGINSPQLLVDSIQIFAAORYSVLNAVOTVGN

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PIYDGLSEANQ"

BASE COUNT 451 a 848 c 630 g 479 t

ORIGIN

Query Match 32.2%; Score 483; DB 8; Length 2408;

Best Local Similarity 99.4%; Pred. No. 1.5e-240;

Matches 683; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 168 CATGCTCAAGTCCACTAGTATCCATGGCAGCGCTTCTCCAGGAGGACCAACTGGGC 227

DB 917 CATGCTCAAGTCCACTAGTATCCATGGCAGCGCTTCTCCAGGAGGACCAACTGGGC 976

QY 228 AGACGAGCCGGTTCGTCACACAGTGCCTATTGCTTCGGGCATTCATTTCTGTACGA 287

DB 977 AGACGAGCCGGTTCGTCACACAGTGCCTATTGCTTCGGGCATTCATTTCTGTACGA 1036

QY 288 CTTCCATGTGCCCCAGCAGGACGAGTCTTGGTACCACAGTCATCTCTCTACGCAATA 347

DB 1037 CTTCCATGTGCCCCAGCAGGACGAGTCTTGGTACCACAGTCATCTCTCTACGCAATA 1096

QY 348 CTGTGACGGGTCGAGGACCGTTCGTCTGTACAGCCCAAGGATCCCGCAGCGCG 407

DB 1097 CTGTGACGGGTCGAGGACCGTTCGTCTGTACAGCCCAAGGATCCCGCAGCGCG 1156

QY 408 CTACGATGTTGACACGAGGACGCTCATCAGTTGACCGACTGGTACACACCGCTGC 467

DB 1157 CTACGATGTTGACACGAGGACGCTCATCAGTTGACCGACTGGTACACACCGCTGC 1216

QY 468 CCGGCTCGGTCCAGGTTCCCACTCGGCGGAGCGCCAGCTCATCAATGGTCTTGGGCG 527

DB 1217 CCGGCTCGGTCCAGGTTCCCACTCGGCGGAGCGCCAGCTCATCAATGGTCTTGGGCG 1276

QY 528 GTCGGCTCCACTCCACCGCGCGTCTGTGTATCAACGTCACGTCACGGAAGGCTA 587

DB 1277 GTCGGCTCCACTCCACCGCGCGTCTGTGTATCAACGTCACGTCACGGAAGGCTA 1336

QY 588 CCGCTTCGGTTCGTTTCGATCTCGTTCGACCCGGAACCTACAGTTACAGTTCAGCGGCA 647

DB 1337 CCGCTTCGGTTCGTTTCGATCTCGTTCGACCCGGAACCTACAGTTACAGTTCAGCGGCA 1396

QY 648 CAATCTGACCGTCATCGAGGTCGAGGTCATCAACAGCAGGCTCTCCTTGTGACTCTAT 707

DB 1397 CAATCTGACCGTCATCGAGGTCGAGGTCATCAACAGCAGGCTCTCCTTGTGACTCTAT 1456

QY 708 CCAGATCTTCGCGCGGAGCGCTACTCCTTGTGTTGAATGCGAACCAACGGTCGGCAA 767

DB 1457 CCAGATCTTCGCGCGGAGCGCTACTCCTTGTGTTGAATGCGAACCAACGGTCGGCAA 1516

QY 768 CTACTGGTTCGCGCGGAGCGCTACTCCTTGTGTTGAATGCGAACCGGTCGGCGGGGATCAATC 827

DB 1517 CTACTGGTTCGCGCGGAGCGCTACTCCTTGTGTTGAATGCGAACCGGTCGGCGGGGATCAATC 1576

QY 828 CGCATCTTCGCGCTACCAAGGCGCAC 854

DB 1577 CGCATCTTCGCGCTACCAAGGCGCAC 1603

RESULT 4

TVU44851

LOCUS 2127 bp DNA linear PLN 02-FEB-1996

DEFINITION Trametes versicolor laccase I (lcci) gene, complete cds.

ACCESSION U44851

VERSION U44851.1 GI:1174244

KEYWORDS

Trametes versicolor strain=52J.

ORGANISM

Trametes versicolor

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

Aphyllophorales; Trametes.

REFERENCE 1 (bases 1 to 2127)

AUTHORS Ong,E., Pollock,B. and Smith,M.

Direct Submission

Submitted (08-JAN-1996) Brent Pollock, Biotechnology Lab, Univ. of

British Columbia, 2125 East Mall, Vancouver, BC V6T 1Z3, Canada

lcci cDNA GenBank Accession #U44430.

COMMENT

Location/Qualifiers

1..2127

/organism="Trametes versicolor"

/strain="52J"

/db_xref="taxon:5325"

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978..1134,1189..1386,1451..1507,1564..1770,1831..2127)

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Number U44430; phenol oxidase"

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/translation="MGLQRFSEFVTLVARSLAAGFVASFVAVNAPVSPDGLRDA

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PAAGDNVTRFQDTNGLGFWFLCHIDFHLFAEIVFAEDVADVKAANVPVKAWSDLG

PIYDGLSEANQ"

BASE COUNT 394 a 721 c 549 g 463 t

ORIGIN

Query Match 19.1%; Score 287; DB 8; Length 2127;

Best Local Similarity 100.0%; Pred. No. 3.5e-138;

Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 CACGCTTCGCGGTTCGTCGAGCGGGGAGCACCACGCTATTAACCTACACGCCGATC 1263

DB 1831 CACGCTTCGCGGTTCGTCGAGCGGGGAGCACCACGCTATTAACCTACACGCCGATC 1890

QY 1324 CAGACGACAAACCCCGCGTGTCTCTCCACTGCCACATCGACTTCCACCTCGACGCG 1383
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Db 2316 CAGACGACAAACCCCGCGTGTCTCTCCACTGCCACATCGACTTCCACCTCGACGCA 2375
|||||
QY 1384 GCGTTCGCGATCGTGTTCGAGAGGAGCTTGGCGGACGTGAAGCGGGGAACCCGGTTCCG 1443
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Db 2376 GCGTTCGCGATCGTGTTCGAGAGGAGCTTGGCGGACGTGAAGCGGGGAACCCGGTTCCG 2435
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QY 1444 AAGCGTGTTCGACCTGTCCCGATCTACGACGGGTGAGCGGCTAACCACTGA 1500
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Db 2436 AAGCGTGTTCGACCTGTCCCGATCTACGACGGGTGAGCGGCTAACCACTGA 2492
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RESULT 6
I65230
LOCUS I65230 2880 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5667531.
ACCESSION I65230
VERSION I65230.1 GI:2481800
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2880)
AUTHORS Yaver,D.Sue., Xu,F., Dalb.o slashed.ge.H., Schneider,P. and Aaslyng,D.A.
TITLE Dye compositions containing purified polyporus laccases and nucleic acids encoding same
JOURNAL Patent: US 5667531-A 3 16-SEP-1997;
FEATURES Location/Qualifiers
source 1..2880
BASE COUNT 547 a 908 c 793 g 632 t
ORIGIN
Query Match 16.4%; Score 246; DB 6; Length 2880;
Best Local Similarity 99.7%; Pred. No. 8.9e-117;
Matches 296; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1204 CACGCTTCGGGTCGTTCGAGCGGGGGAGCACCAGTATACTACAGGACCCGATC 1263
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Db 2196 CACGCTTCGGGTCGTTCGAGCGGGGGAGCACCAGTATACTACAGGACCCGATC 2255
|||||
QY 1264 TTCGCGACGTCGTGAGCAGCGGCACGCCCGCGGGGCAACGTCACGATCCGCTTC 1323
|||||
Db 2256 TTCGCGACGTCGTGAGCAGCGGCACGCCCGCGGGGCAACGTCACGATCCGCTTC 2315
|||||
QY 1324 CAGACGGACAAACCCCGCGTGTCTCTCCACTGCCACATCGACTTCCACCTCGACGCG 1383
|||||
Db 2316 CAGACGGACAAACCCCGCGTGTCTCTCCACTGCCACATCGACTTCCACCTCGACGCA 2375
|||||
QY 1384 GCGTTCGCGATCGTGTTCGAGAGGAGCTTGGCGGACGTGAAGCGGGGAACCCGGTTCCG 1443
|||||
Db 2376 GCGTTCGCGATCGTGTTCGAGAGGAGCTTGGCGGACGTGAAGCGGGGAACCCGGTTCCG 2435
|||||
QY 1444 AAGCGTGTTCGACCTGTCCCGATCTACGACGGGTGAGCGGCTAACCACTGA 1500
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Db 2436 AAGCGTGTTCGACCTGTCCCGATCTACGACGGGTGAGCGGCTAACCACTGA 2492
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RESULT 7
AX015224
LOCUS AX015224 7986 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO9951757.
ACCESSION AX015224
VERSION AX015224.1 GI:10041257
KEYWORDS Trametes versicolor.
SOURCE Trametes versicolor.
ORGANISM Trametes versicolor.
REFERENCE 1 (bases 1 to 7986)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphylliphorales; Trametes.

AUTHORS Pfaller,R., Van Den Hondel,C., Van Gorcom,R. and Hensing,J.
TITLE Expression system for producing proteins
JOURNAL Patent: WO 9951757-A 1 14-OCT-1999;
PFALLER RUPERT (DE); CONSORTIUM ELEKTROCHEM IND (DE); DEN HONDEL CORNELIS VAN (NL); GORCOM ROBERTUS VAN (NL); HESSING JOHANNA (NL)
FEATURES Location/Qualifiers
source 1..7986
/organism="Trametes versicolor"
/db_xref="taxon:5325"
BASE COUNT 1698 a 2404 c 2107 g 1777 t
ORIGIN
Query Match 10.5%; Score 158; DB 6; Length 7986;
Best Local Similarity 100.0%; Pred. No. 7.7e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 584 GCTACCGCTTCGCTCGCTTCGATCTCGTGGCAGCCGGAACCTACAGCTTCAGCATCGACG 643
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Db 2170 GCTACCGCTTCGCTCGCTTCGATCTCGTGGCAGCCGGAACCTACAGCTTCAGCATCGACG 2229
|||||
QY 644 GGCACAATCTGACCGTCATCGAGGTGCAGCGTATCAACAGCCAGCCTCTCCTTGTGACT 703
|||||
Db 2230 GGCACAATCTGACCGTCATCGAGGTGCAGCGTATCAACAGCCAGCCTCTCCTTGTGACT 2289
|||||
QY 704 CTATCCAGATCTTCGGCGCGCAGCGCTACTCTTTGTG 741
|||||
Db 2290 CTATCCAGATCTTCGGCGCGCAGCGCTACTCTTTGTG 2327
|||||
RESULT 8
PGU65399
LOCUS PGU65399 2700 bp DNA linear PLN 19-JUL-1997
DEFINITION Basidiomycete CECT 20197 phenoloxidase (pox1) gene, complete cds.
ACCESSION U65399
VERSION U65399.1 GI:2264395
KEYWORDS basidiomycete CECT 20197.
SOURCE basidiomycete CECT 20197
ORGANISM basidiomycete CECT 20197
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphylliphorales; Polyporaceae.
REFERENCE 1 (bases 1 to 2700)
AUTHORS Mansur,M., Suarez,T., Fernandez-Larrea,J.B., Brizuela,M.A. and Gonzalez,A.B.
TITLE Identification of a laccase gene family in the new lignin-degrading basidiomycete CECT 20197
JOURNAL Appl. Environ. Microbiol. 63 (7), 2637-2646 (1997)
MEDLINE 97355933
PUBMED 9212414
REFERENCE 2 (bases 1 to 2700)
AUTHORS Mansur,M.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1996), Molecular Microbiology, Biological Research Center (CIB), Consejo Superior de Investigaciones Cientificas, Velazquez 144, Madrid 28006, Spain
FEATURES Location/Qualifiers
source 1..2700
/organism="basidiomycete CECT 20197"
/strain="CECT 20197"
/db_xref="taxon:51095"
301..2369
/gene="pox1"
join(301..480,534..602,656..776,839..952,1006..1069,
1125..1220,1280..1436,1494..1691,1756..2019,2073..2369)
/gene="pox1"
/EC_number="1.10.3.2"
/note="laccase; blue-copper oxidase"
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VYVGVPPGLITGKKDQFQLADNLTNHTMLKSTSIHWGFFGAGTWNADGPV
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DESTVITLSDMYHTAATLGLSGRIGADATLINGLGRSSSTPTANTVTINVOHKRYRE
RVLSLSCDNHTFSDGHNLFVIEDVGNKSPLETVDSIOIFAAQKYSFVLNANQVGN
YWRANPFGTFRAGGINSAILRQCAPTEPTVQITTSYIPLVETNLHLLPLVPIPV
GLPVSQVDKALNGFNENFTNNATFTPTVPLVLLQILSGASTAODLLPPGSGV
PLPASHSEITLPAITLAPGAPPHLGHVFAVVRSGASTAYNVDIFRDVYSTGT
PAAGDNVIRFHTDNPFGFWFLHCHIDFLEAGFAIVFAEDVADVKRAANPVPKAWSLDC
PTYDALAESGDL"

BASE COUNT 573 a 834 c 672 g 621 t

Query Match 3.9%; Score 59; DB 8; Length 2700;
Best Local Similarity 100.0%; Pred. No. 4e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 CACTGGCAGCGTCTTCAGGAGGACACCACTGGCAGAGCGACCGCGTTCGTCAA 248
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Db 656 CACTGGCAGCGTCTTCAGGAGGACACCACTGGCAGAGCGACCGCGTTCGTCAA 714
|||||

RESULT 9
AF176230 1829 bp mRNA linear PLN 01-SEP-2000
LOCUS
DEFINITION Polyporus ciliatus laccase (lcc3-1) mRNA, complete cds.
ACCESSION AF176230
VERSION AF176230.1 GI:9957142
KEYWORDS
SOURCE Polyporus ciliatus.
ORGANISM Polyporus ciliatus

REFERENCE
AUTHORS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
TITLE Aphyllophorales; Polyporaceae; Polyporus.
JOURNAL 1. (bases 1 to 1829)
REFERENCE Schnee.C. and Eggert.C.
AUTHORS Isolation and characterization of three laccase genes from the
TITLE white-rot fungus Polyporus ciliatus and their expression during
JOURNAL fruiting
REFERENCE Unpublished
AUTHORS 2. (bases 1 to 1829)
TITLE Schnee.C. and Eggert.C.
JOURNAL Direct Submission

REFERENCE Submitted (06-AUG-1999) Institute of General Microbiology and
AUTHORS Microbial Genetics, Friedrich-Schiller University Jena, Neugasse
TITLE 24, Jena 07743, Germany
JOURNAL Location/Qualifiers
FEATURES
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1. .1829
/organism="Polyporus ciliatus"
/strain="Th1"
/db_xref="taxon:134555"
/tissue_type="vegetative mycelia"
gene
1. .1829
/gene="lcc3-1"
CDS
72..1628
/gene="lcc3-1"
/EC_number="1.10.3.1"
/note="p-phenol oxidase"
/codon_start=1
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/db_xref="GI:9957143"

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DDDSVITLADMYHVAALKLPREPSSDNLINGLGRSPSTADLAVISYTGKRYR
PRLVSLCDPNYTESIDGHQTLVTEADGISQTPVGTGDSIQIFAAQRYSFVLTAQDPV
DNWVRANPFGNTGFAFGINSAILRQYDGAIEPTTNOTGNTLNLELLELHLLPFTTPV
PCNPTQGGADENLNIAFNENFTNNATFTPTVPLVLLQILSGASTAODLLPPGSGV
YALPNSNIEITFATAAAGAPHFLHGHAFVVRSGASTAYNVDIFRDVYSTGT
TPGDNVTIRFHTDNPFGFWFLHCHIDFLEAGFAIVFAEDIPDVASANPVPKAWSLDCP
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BASE COUNT 349 a 622 c 427 g 431 t

Query Match 2.7%; Score 41; DB 8; Length 1829;
Best Local Similarity 100.0%; Pred. No. 1e-09;

MATCHES 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACATCGACATCGACTCCACCTCGAGC 1382
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Db 1470 CCGTGGTTCCTCCACATCGACATCGACTCCACCTCGAGC 1510
|||||

RESULT 10
AF414109 1563 bp mRNA linear PLN 26-SEP-2001
LOCUS
DEFINITION Trametes versicolor laccase B precursor (lac1) mRNA, complete cds.
ACCESSION AF414109
VERSION AF414109.1 GI:15778441
KEYWORDS
SOURCE Trametes versicolor.
ORGANISM Trametes versicolor

REFERENCE 1. (bases 1 to 1563)
AUTHORS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
TITLE Aphyllophorales; Trametes.
JOURNAL Jolivald,C., Madzak,C., Caminade,E. and Mouglin,C.
REFERENCE 2. (bases 1 to 1563)
AUTHORS Jolivald,C., Madzak,C., Caminade,E. and Mouglin,C.
TITLE Direct Submission

REFERENCE Submitted (23-AUG-2001) unite de Phytopharmacie, INRA, Route de
AUTHORS Saint Cyr, Versailles 78026, France
TITLE Location/Qualifiers
JOURNAL 1. .1563
REFERENCE /organism="Trametes versicolor"
AUTHORS /strain="ATCC 32745"
TITLE /db_xref="ATCC:32745"
JOURNAL /db_xref="taxon:5325"
REFERENCE 1. .1563
AUTHORS /gene="lac1"
TITLE /gene="lac1"
JOURNAL 1. .1563
REFERENCE /EC_number="1.10.3.2"
AUTHORS /note="oxidoreductase; induced by 2,5-xyllidine"
TITLE /codon_start=1
JOURNAL /product="laccase B precursor"
REFERENCE /protein_id="AAL07440.1"
AUTHORS /db_xref="GI:15778442"

BASE COUNT 273 a 591 c 387 g 309 t

Query Match 2.5%; Score 38; DB 8; Length 1563;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 CCGTGGTTCCTCCACATCGACATCGACTTCACCTCGA 1379
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Db 1405 CCGTGGTTCCTCCACATCGACATCGACTTCACCTCGA 1442
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RESULT 11
AB006824 1739 bp mRNA linear INV 03-JUN-1998
LOCUS
DEFINITION Trachyderma tsunodae mRNA for Billrubin Oxidase, complete cds.
ACCESSION AB006824


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VERSION AB006824.1 GI:3176127
KEYWORDS Bilirubin Oxidase.
SOURCE Trachyderma tsunodae (strain:K-2593) cDNA to mRNA.
ORGANISM Trachyderma tsunodae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Trachyderma.
REFERENCE
AUTHORS Iwamoto,H., Watanabe,H., Minakami,M., Hirose,J., Hiromi,K.,
Mukai,H., Yoshioaka,H. and Kato,I.
TITLE Purification, Characterization, and Molecular Cloning of Bilirubin
Oxidase from Trachyderma tsunodae K-2593
JOURNAL Unpublished
REFERENCE
AUTHORS Iwamoto H.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1997) Hiroyuki Iwamoto, Fukuyama University,
Faculty of Engineering, Gakuen-cho, Fukuyama, Hiroshima 729-02,
Japan (E-mail:iwamoto@fubac.fukuyama-u.ac.jp, Tel:0849-36-2111,
Fax:0849-36-2023)
FEATURES
source 1..1739
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13..1578
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DNDSTVITLADWVAARLGRPLGASVINGLGRSLSTPNADLAVISVTOGKRYR
FRLLISCDPFHFSIDCHLTIIEADSVNTEPLVDAIPFAGQKYSFVLSAVKIDID
NYWIRADPGFTTGAGINSAILRDYGAAPTEPTAVLAPVSNPLVETDLHLEMDP
VQRPRTKGGYKAINLDFSEFFNFINNATFTSPVPIILQIMSGAQAQDILLPSGS
VIELPAQSTIELLPATVNAAGVPVPHFHLHGHTFAVVRSGASTAYNDNPIMRDVYST
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13..75
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polyA_signal 1717..1722
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polyA_site 1739
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BASE COUNT 351 a 587 c 416 g 385 t
ORIGIN
Query Match 2.5%; Score 38; DB 3; Length 1739;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
|||||
DB 1420 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1457
|||||
RESULT 12
AF491759 AF491759 1869 bp mRNA linear PLN 09-APR-2002
LOCUS Basidiomycete C30 lacase 1 (lac1) mRNA, complete cds.
DEFINITION AF491759
ACCESSION AF491759
VERSION AF491759.1 GI:20086990
KEYWORDS basidiomycete C30.
SOURCE basidiomycete C30
ORGANISM basidiomycete C30
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; unclassified Coriolaceae.
REFERENCE
AUTHORS Iwamoto,H. and Tron,T.
TITLE clac1, the cDNA encoding the LAC1 from the basidiomycete C30
JOURNAL Unpublished
REFERENCE
AUTHORS Klonowska,A. and Tron,T.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2002) Chemistry, LBS UMR 6517 CNRS, Avenue
Escadrille Normandie-Niemen, Marseille 13397, France
FEATURES
source 1..1869
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42..1595
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Accession Number AF162785"
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/db_xref="GI:20086991"
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DDSTVITLADWVAARLGRPLGASVINGLGRSLSTPNADLAVISVTOGKRYR
RLVSLCDPNHTEIDGHSFLVTEADSVNLKPTQVDSIQIFAAQRYSFVLNADQVDN
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SIPANADIIEISLPATSAAGFPFPHFHLHGHTFAVVRSGASTAYNDNPIMRDVYSTGS
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1819..1824
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1841
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polyA_signal 364 a 631 c 466 g 408 t
polyA_site 631 c
BASE COUNT 364 a 631 c 466 g 408 t
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Query Match 2.5%; Score 38; DB 8; Length 1869;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1342 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1379
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DB 1437 CCGTGGTTCCTCCACTGCCACATCGACTTCCACCTCGA 1474
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RESULT 13
AF176231 AF176231 2020 bp mRNA linear PLN 01-SEP-2000
LOCUS Polyporus ciliatus lacase (lcc3-2) mRNA, complete cds.
DEFINITION AF176231
ACCESSION AF176231
VERSION AF176231.1 GI:9957144
KEYWORDS Polyporus ciliatus.
SOURCE Polyporus ciliatus
ORGANISM Polyporus ciliatus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Polyporaceae; Polyporus.
REFERENCE
AUTHORS Schnee,C. and Eggert,C.
TITLE Isolation and characterization of three laccase genes from the
white-rot fungus Polyporus ciliatus and their expression during
fruiting
JOURNAL Unpublished
REFERENCE
AUTHORS Schnee,C. and Eggert,C.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) Institute of General Microbiology and
Microbial Genetics, Friedrich-Schiller University Jena, Neugasse
```


24, Jena 07743, Germany												
Location/Qualifiers												
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71..1645												
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BASE COUNT		389 a		712 c		468 g		451 t				
ORIGIN												
Query Match 2.5%; Score 38; DB 8; Length 2020;												
Best Local Similarity 100.0%; Pred. No. 3.7e-08;												
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;												
QY 1342		CCGTGTTCTCCACATGCCACATCGACTTCCACCTCGA 1379 										
Db 1481		CCGTGTTCTCCACATGCCACATCGACTTCCACCTCGA 1518 										
RESULT 14												
AF388910												
LOCUS												
DEFINITION White-rot fungus AH28-2 laccase gene, partial sequence.												
ACCESSION AF388910												
VERSION AF388910.1 GI:14669597												
KEYWORDS												
SOURCE white-rot fungus AH28-2.												
ORGANISM Eukaryota; Fungi; Basidiomycota.												
REFERENCE 1 (bases 1 to 2043)												
AUTHORS Xiao,Y., Wu,J. and Shi,Y.												
TITLE Cloning of laccase gene from a new white-rot fungus AH28-2												
JOURNAL Unpublished												
REFERENCE 2 (bases 1 to 2043)												
AUTHORS Xiao,Y., Shi,Y., Chen,Q., Wang,J., Hang,J., Wu,J., Wang,Y., Jia,R. and Zhang,M.												
TITLE Direct Submission												
JOURNAL Submitted (02-JUN-2001) School of Life Science, Anhui University, 3 Feixi Road, Hefei, Anhui 230039, P.R. China												
FEATURES												
Location/Qualifiers												
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/strain="AH28-2"												
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Best Local Similarity 100.0%; Pred. No. 3.7e-08;												
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;												
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Db 1888		CCGTGTTCTCCACATGCCACATCGACTTCCACCTCGA 1925 										
RESULT 15												
TMTLCCA												
LOCUS												
DEFINITION Trametes villosa (clone LCC1) laccase gene, exons 1-9, complete cds												
ACCESSION L49376												
VERSION L49376.1 GI:1100243												
KEYWORDS laccase.												
SOURCE Trametes villosa												
ORGANISM Trametes villosa (clone: LCC1) vegetative growth mycelia DNA. Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Trametes.												
REFERENCE 1 (bases 1 to 2417)												
AUTHORS Iaver,D.S., Xu,F., Golightly,E.J., Brown,K.M., Brown,S.H., Rey,M.W., Schneider,P., Halkier,T., Mondor,K. and Dalboge,H.												
TITLE Purification, characterization, molecular cloning, and expression of two laccase genes from the white rot basidiomycete Trametes villosa												
JOURNAL Appl. Environ. Microbiol. 62 (3), 834-841 (1996)												
MEDLINE 97076915												
PUBMED 8975623												
FEATURES												
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/dev_stage="vegetative growth"												
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533..588												
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589..709												
/gene="lcc1"												
/number=3												
710..764												
intron												

